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5.1.6
Compugen Ltd.
version 9
GenCore
Copyright (c) 1993
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protein search, using sw model OM protein -

March 31, 2005, 02:17:12; Search time 88.7903 Seconds (without alignments) 65.338 Million cell updates/sec Run on:

US-10-056-583A-64 70 Title: Perfect score:

1 EAAKYEAYKAAAAA 15 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

A_Geneseq_16Dec04:* Database

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•		0 HLA-DR2 m	1 HLA-DR2 m	2 HLA-DR2 m	8 HLA-DR2 m		6 HLA-DR2 m	5 HLA-DR2 m	7 HLA-DR2 m	0 HLA-DR2 m	1 HLA-DR2 m	2 HLA-DR2 m	9 HLA-DR2 m	7 HLA-DR2 m	3 HLA-DR2 m	1 HLA-DR2 m	4 HLA-DR2 m	3 HLA-DR2 m	1 HLA-DR2 m	51 HLA-DR2 m	8 HLA-DR2 m	8 HLA-DR2 m	9 HLA-DR2 m	5 HLA-DR2 m	O HLA-DR2 m	1 HLA-DR2 m
	Description	Abp5227	Abp5227	Abp5227	Abp52296	Abp5229	Abp52296	Abp5229	Abp5225	Abp5229	Abp5226	Abp5229	Abp5226	Abp5226	Abp5226	Abp5230	Abp5230	Abp5230	Abp5229	Abp5225	Abp5224	Abp5226	Abp5223	Abp5226	Abp5224	Abp5224
		ABP52270	ABP52271	ABP52272	ABP52298	ABP52294	ABP52296	ABP52295	ABP52257	ABP52290	ABP52261	ABP52292	ABP52269	ABP52267	ABP52263	ABP52301	ABP52304	ABP52303	ABP52291	ABP52251	ABP52248	ABP52268	ABP52239	ABP52265	ABP52240	ABP52241
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do	ក្នុង	100.0	92.9	92.9	92.9	92.9	92.9	92.9	91.4	85.7	85.7	85.7	85.7	84.3	84.3	81.4	80.0	80.0	78.6	78.6	78.6			77.9	77.1	77.1
	Score	70	65	65	65	65	65	65	64	9	9	9	9	59	59	57	26	95	52	52	52	52	55		54	54
	Result No.		7	m	4	ß	9	7	8	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

HLA-HLA-HLA-HLA-HLA-HLA-HLA-HLA-HLA-HLA-	ADDSZZOB HLA-DKZ Adj57542 Cop-1 rel Adg59601 Copolymer
5 ABP52249 5 ABP52243 5 ABP52258 5 ABP52259 5 ABP52260 5 ABP52360 5 ABP52305 5 ABP52360 5 ABP52255 5 ABP52255 5 ABP52255 5 ABP52257 6 ABP52257 7 AAY82058 7 AAY82058 7 ABP52256 7 ABP52256 7 ABP52256	5 ABF32286 7 ADJ57542 8 ADQ59601
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ALIGNMENTS

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent. HLA-DR2 molecule binding peptide SEQ ID NO:64. ABP52270 standard; peptide; 15 AA (first entry) 16-OCT-2002 ABP52270; ABP52270 ID ABP

Homo sapiens. Synthetic. WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P

(HARD) HARVARD COLLEGE

Ξ Strominger JL, Fridkis-Hareli

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

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demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
encephalomyelitis, a post-vaccine
      sclerosis,
      multiple
                                                                                                                                               Sequence 15 AA;
      such as multig
demyelinating
                                                                                                        invention
        8X8888XX
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ö Score 70; DB 5; Length 15; Pred. No. 8.6e-05; Mismatches 0; Indels . 0 Query Match Best Local Similarity 100.0%; Matches 15; Conservative 0; 1 EAAKYEAYKAAAAA 15 EAAKYEAYKAAAAA 15 8 8

ABP52271 standard; peptide; 15 AA RESULT 2 ABP52271

(first entry) 16-OCT-2002 ABP52271;

HLA-DR2 molecule binding peptide SEQ ID NO:65.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent post-viral

sapiens Synthetic. Ношо

WO200259143-A2

01-AUG-2002

24-JAN-2002; 2002WO-US002071

24-JAN-2001; 2001US-0263569P

(HARD) HARVARD COLLEGE

Fridkis-Hareli Strominger JL,

WPI; 2002-608439/65.

Σ̈́

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                 Gaps
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Length 15;
                 1; Indels
Score 65; DB 5; 1
Pred. No. 0.00057;
                  Mismatches
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  92.98;
           93.3%;
                   14; Conservative
           Similarity
  Query Match
Best Local S
                   Matches
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Sequence 15 AA;

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1 EAAKYEAYKAAAAA 15

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ABP52272 standard; peptide; 15 AA.

RESULT 3 ABP52272

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Gaps

ABP52272;

(first entry) 16-OCT-2002 HLA-DR2 molecule binding peptide SEQ ID NO:66.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;

anti-tumour necrosis factor agent

Homo sapiens. Synthetic.

WO200259143-A2

01-AUG-2002.

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Ξ Strominger JL, Fridkis-Hareli

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English

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Sequence 15 AA;

Gaps .. 0 92.9%; Score 65; DB 5; Length 15; 93.3%; Pred. No. 0.00057; ive 0; Mismatches 1; Indels 14; Conservative Query Match Best Local Similarity Best Loc Matches

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1 EAAKYEAYKAAAAA 15

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16-OCT-2002 (first entry)

ABP52294;

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52205 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                          Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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Pred. No. 0.00057;
0; Mismatches 1; Indels
                                                                                                      HLA-DR2 molecule binding peptide SEQ ID NO:92.
ABP52298 standard; peptide; 15 AA
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Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                           Synthetic.
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                               Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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Pred. No. 0.00065;
); Mismatches 1; Indels
                                                                                 HLA-DR2 molecule binding peptide SEQ ID NO:88.
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                                                                                                                                                                                                     anti-tumour necrosis factor agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strominger JL, Fridkis-Hareli M;
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Local Similarity 93.3%;
Les 14; Conservative (
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Gaps

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                   New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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                                                                                           anti-tumour necrosis factor agent
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                                                                                                                                                                                                                                                                                                                                                                Fridkis-Hareli
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                                                                                                                              Homo sapiens.
Synthetic.
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ABP52295
ID ABP5
XX
AC ABP5
XX
DT 16-(
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DE HLA
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KW HLA
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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Pred. No. 0.00073;
0; Mismatches 1; Indels
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                                                                                                                                                                                                       Fridkis-Hareli
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                                                                                                                                        24-JAN-2001; 2001US-0263569P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 92.9%;
11 Similarity 93.3%;
14; Conservative
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                  encephalomyelitis.
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                  Synthetic.
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HLA-DR2 molecule binding peptide SEQ ID NO:84.
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                                                                                         Example 1; Page 32; 54pp; English.
                                   Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                                                                                                     ABP52290 standard; peptide; 15
24-JAN-2002; 2002WO-US002071
           24-JAN-2001; 2001US-0263569P.
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Strominger JL, Fridkis-Hareli M;

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
                                                                                                    New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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Pred. No. 0.00083;
0; Mismatches 1; Indels
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Gaps

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                                                                                  The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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Pred. No. 0.0037;
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                                  Example 1; Page 33; 54pp; English
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86.7%;
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1es 13; Conservative
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ABP52292
XX
AC ABP52
XX
DE HLA-D
XX
HUMAN
KW HLA-D
KW HLA-D
KW HLA-D
KW HLA-D
KW MHC C
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

Claim 28; Page 39; 54pp; English.

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immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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Pred. No. 0.0037;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP52269 standard; peptide; 15 AA
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Best Local Similarity 86.7
Matches 13; Conservative
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                        Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
represent peptides used in the exemplification of the present
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3. 0.0037; ...haa 1; Indels
                                                                                      5; Length 15;
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                                                                                  85.7%; Score 60; DB
86.7%; Pred. No. 0.00
iive 1; Mismatches
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                                                                                                                                                     1 EAAKYEAYKAAAAA 15
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EAAYKAYKAAAAA 15
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                                                                                                                    Conservative
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                                                                                                  Local Similarity
Les 13; Conserv
                                                 Sequence 15 AA;
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 ABP52305
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Matches
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Score 59; DB 5; Length 15; Pred. No. 0.0055;

84.3%;

Query Match Best Local Similarity

Sequence 15 AA;

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                                                                                                                                                                                                                                                                                      Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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86.7%; Pred. No. 0.0055;
iive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                     HLA-DR2 molecule binding peptide SEQ ID NO:57.
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          anti-tumour necrosis factor agent
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                                  1 EAAKYEAYKAAAAA
                                                                1 EAKAYEAYKAAAAA
13; Conservative
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                              HLA-DR2 molecule binding peptide SEQ ID NO:95.
                                                                                 ABP52301 standard; peptide; 15 AA
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                                                                                                                                                                     ABP52301;
RESULT 15
ABP52301
ID ABP52301
DXX ABP52301
DXX ABP52301
DXX Human
KW HLA-D
XX Homo
DX HOMO
DX HOMO
DX Synth
XX ABP52
DX ABP52
DX HOMO
DX HOMO
DX ABP52
CC COMPI
CC C
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Query Match 81.4%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.012;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EAAKYEAYKAAAAAA 15

1 EAAKYEAYKAAAAA 15 | ||:||:||:||||| 1 EKAKFEAFKAAAAA 15

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Search completed: March 31, 2005, 02:35:27 Job time: 89.7903 secs

us-10-056-583a-64.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds (without alignments)
48.718 Million cell updates/sec OM protein - protein search, using sw model 1 EAAKYEAYKAAAAAA 15 US-10-056-583A-64 70 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

513545 segs, 74649064 residues

Searched:

513545

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result					
Score	e Match	Length	DB	ID	Description
4	 	13	່ທ	PCT-US95-04121-38	Sequence 38, Appl
4	0 57.1	. 13	ഗ	PCT-US94-10257A-33	33,
4	0	391	4	US-09-902-540-11110	1111
4	0 57.1	466	4	US-09-489-039A-13950	Sequence 13950, A
	Ŋ		-	US-07-988-754-4	4
39.	ß		-1	US-07-988-754-12	Sequence 12, Appl
m	თ	186	4	US-09-902-540-11242	=
m			~	08-836-	7
m			4	US-09-252-991A-21824	2182
m			4	-09-252-	Sequence 18769, A
38.	Z,	98	4	9-405-	6,
ø	53 S		4	US-09-816-989A-6	
m		64	4	US-09-248-796A-26627	266
m	œ	407	4	US-09-252-991A-29581	
m			4	US-09-252-991A-32086	
m		20	Н	US-08-440-861-23	
m			v	5169933-42	Patent No. 5169933
ო	7 52.9		9	5169933-42	Patent No. 5169933
m	7 52.9		4	US-09-405-743A-7	Sequence 7, Appli
M			4	US-09-816-989A-7	7,
m				US-08-440-861-2	7
m			-1	-08 - 433	7
m	7		7	US-08-174-745A-2	Sequence 2, Appli
m	7		~	8-195	7
٣	7		N	US-08-433-885-2	2,
m	7 52.9	301	~	-08-433	Sequence 2, Appli
m	7 52.9		ო	US-08-410-614-2	2

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PCT-US94-10257A-33; Sequence 33, Application PC/TUS9410257A; GENERAL INFORMATION: APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION

| |:| ||||||| 1 AAYKAAKAAAAA 13

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3 AKYEAYKAAAAA 15

Sequence 46186, A	Sequence 48, Appl	Sequence 48, Appl	Sequence 2, Appli	Sequence 3940, Ap	Sequence 4256, Ap	Sequence 5116, Ap	Sequence 6, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 11230, A	Sequence 18658, A	Sequence 11523, A	Sequence 11524, A	Sequence 60, Appl	Sequence 42, Appl	Sequence 2, Appli	Sequence 2, Appli
US-09-270-767-46186	US-08-961-083-48	US-09-536-784-48	US-09-196-857-2	US-09-583-110-3940	US-09-107-433-4256	US-09-543-681A-5116	US-08-295-670-6	US-08-633-485-6	US-08-508-761B-4	US-09-489-039A-11230	US-09-248-796A-18658	US-09-949-016-11523	US-09-949-016-11524	PCT-US95-04121-60	US-09-117-121-42	US-09-405-743A-2	US-09-816-989A-2
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400	426	426	427	427	435	459	497	497	510	802	1001	741	741	13	37	45	45
52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.1	52.1	51.4	51.4	51.4	51.4
37	37	37	37	37	37	37	37	37	37	37	37	36.5	36.5	36	36	36	36
28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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0
                                   Sequence 38, Application PC/TUS9504121
; Sequence 38, Application.
; APPLICANT:
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
; NUMBER OF SEQUENCES: 62
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Flopy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 5; Length 13;
Pred. No. 0.82;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,206
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 079.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.0%;
Best Local Similarity 76.9%;
Matches 10; Conservative
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CLASSIFICATION:
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RESULT 1
PCT-US95-04121-38
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RESULT 5
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                 APPLICANT: JONATHAN B. ROTHBARD
APPLICANT: DAWN SMILEK
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-902-540-11110
; Sequence 11110, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Wiegand, Roger C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11110
; LENGTH: 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1 SELECTION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,824
FILING DATE: 03-SEP-1993
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: ANNE I CRAIG
REGISTRATION NUMBER: 32,976
REGISTRATION NUMBER: 071.1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6040
TELEPHONE: (617) 466-6040
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                ZIP: 02145
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10257A
BRIGITTE DEVAUX
JONATHAN B. ROTHBARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.1%;
Best Local Similarity 76.9%;
Matches 10; Conservative
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; ORGANISM: Myxococcus xanthus
US-09-902-540-11110
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                                                                                                                                                                                                                     CITY: WALTHAM STATE: Massachusetts
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                                                                                                                                                                                                                                                                  COUNTRY: USA
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PCT-US94-10257A-33
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Sequence 13950, Application US/09489039A

Sequence 13950, Application US/09489039A

Sequence 13950, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13950

LENGTH: 466
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                                                    Gaps
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Score 40; DB 4; Length 391;
Pred. No. 59;
3; Mismatches 4; Indels
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Creative Biomolecules
ADDRESSE:
Creative Biomolecules
STREET:
STATE: MA
COUNTRY: U.S.A.
ZIP: 01748
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,754
FILING DATE: 19921210
CLASSIFICATION NUMBER: US/07/627,323
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: CRP-046
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4
Pred. No. 71;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/07988754
Patent No. 5374431
GENERAL INFORMATION:
APPLICANT: Pang, Roy H.L.
APPLICANT: Cohen, Charles M.
APPLICANT: Keck, Peter C.
TITLE OF INVENTION: Synthetic Bloadhesive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13950
Query Match 57.1%;
Best Local Similarity 53.3%;
Matches 8; Conservative
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Best Local Similarity 76.9%;
Matches 10; Conservative
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81 KAEAYRAYKASAGSA 95
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FILING DATE:
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Pred. No. 3.4;
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STREET: 35 South Street
CITY: Hopkinton
STATE: MA
COUNTRY: U.S.A.
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,754
FILING DATE: 19921210
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APPLICANT: Cohen, Charles M.
APPLICANT: Keck, Peter C.
TITLE OF INVENTION: Synthetic Bioadhesive
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Creative Biomolecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19921210
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/627,323
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: CRP-046
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/07988754
Patent No. 5374431
GENERAL INFORMATION:
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TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 21 amino TVDP
                                                                                                                                                                                                                                                 56.4%;
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                                                                 LENGTH: 21 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                           ; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-07-988-754-4
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Best Local Similarity 68.8
Matches 11; Conservative
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Best Local Similarity 68.8
Matches 11; Conservative
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US-07-988-754-12
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                                                                 APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11242
LENGTH: 186
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Pred. No. 40;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
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FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 11242, Application US/09902540 Patent No. 6833447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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48 SASYQKYKAAADA 60
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                                                     GENERAL INFORMATION:
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ORGANISM: RA
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APPLICANT: Lis, Doris TILLS, Doris TILLS, Doris TILLS, Doris TILLS, Doris TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin version 3.1 SEQ ID NO 6 LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2627, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                   Gequence 6 Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 86
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.5; DB
Pred. No. 22;
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Best Local Similarity 73.3%;
Matches 11; Conservative 1
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APPLICANT: Gad, Alexander
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US-09-248-796A-26627
                                                     JS-09-405-743A-6
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Sequence 1875, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18769
LENGTH: 731
                                                                                                                                                                                                                                                                                                                                                    RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-21824
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                                                                                                                                                                                                                                    Sequence 21824, Application US/09252991A; Sequence 21824, Application US/09252991A; Sequence 21824, Application US/09252991A; Sequence 21824, Application US/09252991A; Patent No. 6551795; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATII; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; FILE REFERENCE: 107196.136; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 21824; ENERGING PRIOR FILING DATE: 1998-07-27; SEQ ID NO 21824; SEQ ID NO 21824
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Pred. No. 1.3e+02;
3; Mismatches 2; Indels
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   Pred. No. 1.3e+02;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
Best Local Similarity 66.7%;
Matches 10; Conservative
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Matches 8; Conservative
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US-09-252-991A-21824
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TYPE: PRT
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Sequence 32086, Application US/09252991A
Patent No. 6551708.
Patent No. 6551708.
Patent No. 6551708.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-29581
; Sequence 29581, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
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Pred. No. 1.3e+02;
1; Mismatches 3; Indels
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FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A;
CURRENT APPLICATION NUMBER: US/09/252,991A;
PRIOR APPLICATION NUMBER: US 60/074,788;
PRIOR PILING DATE: 1998-02-18;
PRIOR PILING DATE: 1998-07-27;
NUMBER OF SEQ ID NOS: 33142;
SEQ ID NO 29581;
LENGTH: 407
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                            PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26627

LENGTH: 64
                                        CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581
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Best Local Similarity 71.4%;
Matches 10; Conservative
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263 EAAKKKAAAAAAA 276
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                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.4
Matches 10; Conservative
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US-09-252-991A-32086
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j Tirk: FRT
j ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32086
US-09-252-991A-32086

Query Match
Best Local Similarity 64.3%; Score 38; DB 4; Length 534;
Best Local Similarity 64.3%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EAAKYEAYKADAAA 14

Qy 1 EAAKYEAYKADAAA 345

Db 332 EAAHVEAHRADAAA 345

Search completed: March 31, 2005, 02:44:07

Job time: 22.9839 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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74.648 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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1 70 100.0 15 14 US-10-056-583-64 Sequence 64, Appl 2 65 92.9 15 14 US-10-056-583-65 Sequence 66, Appl 6 92.9 17 14 US-10-056-583-88 Sequence 66, Appl 7 14 US-10-056-583-89 Sequence 89, Appl 8 60 85.7 15 14 US-10-056-583-89 Sequence 90, Appl 7 14 US-10-056-583-89 Sequence 91, Appl 8 60 85.7 15 14 US-10-056-583-89 Sequence 51, Appl 10 60 85.7 15 14 US-10-056-583-89 Sequence 51, Appl 11 60 85.7 15 14 US-10-056-583-84 Sequence 63, Appl 11 60 85.7 15 14 US-10-056-583-84 Sequence 86, Appl 11 60 85.7 15 14 US-10-056-583-84 Sequence 86, Appl 11 50 885.7 15 14 US-10-056-583-86 Sequence 86, Appl 11 50 885.7 15 14 US-10-056-583-86 Sequence 87, Appl 12 59 84.3 15 14 US-10-056-583-81 Sequence 57, Appl 13 59 84.3 15 14 US-10-056-583-61 Sequence 61, Appl 11 60 85.7 15 14 US-10-056-583-81 Sequence 62, Appl 11

Sequence 95, Appl Sequence 92, Appl Sequence 97, Appl Sequence 33, Appl Sequence 42, Appl Sequence 42, Appl Sequence 62, Appl Sequence 53, Appl Sequence 34, Appl Sequence 37, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 54, Appl Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 96, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 47, Appl Sequence 49, Appl Sequence 49, Appl Sequence 91, Appl Appl Appl Sequence 91, Appl Appl Appl Appl Appl Appl Appl App	Sequence 24, Appl Sequence 24, Appl Sequence 50, Appl Sequence 60, Appl Sequence 83, Appl Sequence 28, Appl Sequence 26, Appl Sequence 26, Appl
US-10-056-583-95 US-10-056-583-92 US-10-056-583-98 US-10-056-583-97 US-10-056-583-97 US-10-056-583-85 US-10-056-583-85 US-10-056-583-85 US-10-056-583-85 US-10-056-583-85 US-10-056-583-85 US-10-056-583-99	US-09-765-301-24 US-09-765-644A-24 US-10-056-583-50 US-10-056-583-60 US-10-056-583-83 US-10-438-538-28 US-10-056-583-26 US-10-056-583-30
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US-10-056-583-64

is Sequence 64, Application US/10056583

sequence 64, Application No. US20030064915A1

is Publication No. US20030064915A1

is Publication No. US20030064915A1

is APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Harel, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT PILING DATE: 2002-01-24

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 64

LENGTH: 15

TYPE: PRT

TYPE: PRT

TYPE: PRT

CORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-64

Query Match

Best Local Similarity 100.0%; Score 70; DB 14; Length 15;

Best Local Similarity 100.0%; Pred. No. 9e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

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DD I EAAKYEAYKAAAAAA 15
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RESULT 2 US-10-056-583-65

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US-10-056-583-89
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APPLICANT: Presidents and Fellows of Harvard College; APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING; TITLE OF INVENTION: TORNITIONS; FILE REFERENCE: 24655-017; CURRENT APPLICATION NUMBER: US/10/056,583; CURRENT FILING DATE: 2002-01-24; PRIOR APPLICATION NUMBER: 60/263,569; PRIOR FILING DATE: 2001-01-24
                                                                   APPLICANT: Presidents and Fellows of Harvard College;
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.9%; Score 65; DB 14; Length 15; Best Local Similarity 93.3%; Pred. No. 0.00058; Matches 14; Conservative 0; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 15
Sequence 65, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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Matches 14; Conserva
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US-10-056-583-88
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Sequence 88, Application US/10056583; Bublication No. US20030064915A1; GENERAL INFORMATION: APPLICANT: Presidents and Fellows of Harvard College; APPLICANT: Strominger, Jack L.

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Sequence 90, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 17
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 88
LENGTH: 17
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; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
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Sequence 89, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
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Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1;
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Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
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US-10-056-583-63
         SEQ ID NO 55
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Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 51
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Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Strominger, Jack L.

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-51
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CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569.
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 19
                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-056-583-84

Sequence 84, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

FILE REFERENCE: 24655-017

CURRENT FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FASTSEQ for Windows Version 4.0
j LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-55
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Pred. No. 0.0037;
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APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 15
TYPE: PRT
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; Sequence 63, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
                                                                                                                                                                                     Query Match 85.7%;
Best Local Similarity 86.7%;
Matches 13; Conservative
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ORGANISM: Artificial Sequence
PEATURE:
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; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
    APPLICANT: Presidents and Fellows of Harvard College
    APPLICANT: Strominger, Jack L.
    APPLICANT: Fridkis-Hareli, Masha
    TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
    TITLE OF INVENTION: CONDITIONS
    FILE REFERENCE: 24655-017
    FURENT APPLICATION NUMBER: US/10/056,583
    CURRENT APPLICATION NUMBER: 60/263,569
    PRIOR APPLICATION NUMBER: 60/263,569
    PRIOR FILING DATE: 2001-01-24
    NUMBER OF SEQ ID NOS: 99
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 95
    LENGTH: 15
    LENGTH: 15
                                                                                                                                                                                                 Sequence 61, Application US/10056583

Sequence 61, Application World US/20030064915A1

Publication No. US20030064915A1

GENERAL INFORMATION:
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 61

LENGTH: 15
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Best Local Similarity 86.7%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 2; Indels
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   Mismatches
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ORGANISM: Artificial Sequence
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1 EKAKFEAFKAAAAA 15
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     13; Conservative
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US-10-056-583-95
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US-10-056-583-61
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           Matches
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Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

TITLE OF INVENTION: CONDITIONS

TITLE OF INVENTION UNDER: 00/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 86

LENGTH: 15
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Sequence 57, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24
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; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57
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; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 14; Length 15;
Pred. No. 0.0037;
0; Mismatches 2; Indels
                                                                                 Score 60; DB 14; Length 15;
Pred. No. 0.0037;
                                                                                                                                   2; Indels
                                                                                   Query Match 85.7%; Score 60; DB Best Local Similarity 86.7%; Pred. No. 0.00 Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.3%;
86.7%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.7%;
Best Local Similarity 86.7%;
Matches 13; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                           RESULT 11
US-10-056-583-86
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RESULT 12

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RESULT 15
US-10-056-583-92

i Sequence 92, Application US/10056583

j Publication No. US20030064915A1

i GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: UNBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR PILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 92

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

COTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.0%; Score 56; DB 14; Length 15; Best Local Similarity 86.7%; Pred. No. 0.016; Matches 13; Conservative 0; Mismatches 2; Indels
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1 EAAKYEAYKAAAAA 15 g ઠ

Search completed: March 31, 2005, 02:48:48 Job time : 67.5323 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds (without alignments) 80.614 Million cell updates/sec Run on:

US-10-056-583A-64 70

1 EAAKYEAYKAAAAA 15 Sequence:

Perfect score:

Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	42	60.09	188	5	I50145	homeotic protein H
7	42	60.0	254	7	H86355	
m	42	60.09	289	~	A43562	proteir
4	42	60.0	527	7	E69351	phosphoglycerate d
ស	41	58.6	124	~	E84764	hypothetical prote
9	41	58.6	1857	Н	S01787	fatty-acid synthas
7	41	58.6	2129	~	T27431	hypothetical prote
80	40	57.1	251	0	C70521	1-acylglycerol-3-p
თ	40	57.1	354	Н	GNVVSR	genome polyprotein
10	40	57.1	788	~	F97547	probable oxidoredu
11	40	57.1	788	(7	AC2767	formate dehydrogen
12	40	57.1	908	• •	T13690	hypothetical prote
13	40	57.1	1151	N	T18535	high molecular mas
14	39	55.7	101	•	G75512	conserved hypothet
15	39	55.7	170	• •	E81312	probable lipoprote
16		55.7	250	N	T51971	proteasome endopep
17		55.7	519	N	S39893	rnfC protein - Rho
18	39	55.7	553	7	D83640	ŭ
		55.7	599	-	QRMSE	estrogen receptor
		55.7	009	-	QRRTE	estrogen receptor
21		55.7	698	~	T32594	hypothetical prote
		55.7	728	~	H82965	DNA helicase II PA
		54.3	108	N	F97521	VCO33 protein homo
		54.3	108	~	AH2740	conserved hypothet
		٠	261	~	T51222	hypothetical prote
		54.3	E	-	DEECG3	glyceraldehyde-3-p
27		54.3	331	~	AG0711	glyceraldehyde 3-p
		54.3	331	7	D85788	glyceraldehyde-3-p
29		54.3	331	~	H90939	- 1

conserved hypothet	probable fatty-aci	tetrahydrofolylpol	folylpolyglutamate	hypothetical prote	ATPase, AAA family	H+-transporting tw	efflux system prot	related to protein	probable fatty-aci	fatty acid synthas	ribosomal protein	transcription regu	T-cell receptor ga	exoskeletal protei
C82156 F83525	T43037	B81936	C81170	E87463	D87408	S04675	E87470	T49355	T43409	T38781	B87702	G87606	S36290	877930
0.0	ı م	0	N	N	N	N	N	N	N	7	~	7	~	0
346	377	424	424	428	433	478	478	521	1842	1842	165	176	185	189
54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	52.9	52.9	52.9	52.9
8 8	38	38	38	38	38	38	38	38	38	38	37	37	37	37
30	32	. 33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
N;Alternate names: CHOX M
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: ISO145; S14512
R;Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
A;Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic viralisence number: ISO145; MUID:91238215; PMID:1674560
A;Accession: ISO145
```

A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Residues: 1-188 <CRO> A.Cross references: UNIPROT: P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g62701

A;Gene: CHOX M A;Gene: CHOX M C;Superfamily: homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;96-152/Domain: homeobox homology <HOX>

Gaps .. 0 60.0%; Score 42; DB 2; Length 188; 81.8%; Pred. No. 9.8; 2; Indels :ive 0; Mismatches 2; Indels Local Similarity 81.8 es 9; Conservative Query Match Best Loc Matches

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5 YEAYKAAAAAA 15 10 YSKYKAAAAA 20 원 Š

Cypecies: Arabidopsis thaliana
Cyspecies: Arabidopsis thaliana
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86355
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-254 <STO>

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Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative 0
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Best Local Similarity 66.7%;
Matches 8; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-124 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: homeotic protein Hox 4.3
C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562
R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobd A;Reference number: A43562; MUD:91209232; PMID:1982431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphoglycerate dehydrogenase (serA) homolog - Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C; Accession: E69351
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
Nature 390, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-527 <KLE>
A;Cross-references: UNIPROT:029445; GB:AE001048; GB:AE000782; NID:g2689371; PIDN:AAB9042
C;Superfamily: Bacillus phosphoglycerate dehydrogenase
A;Cross-references: UNIPROT:P48347; GB:AE005172; NID:99392684; PIDN:AAF87261.1; GSPDB:GN
C;Genetics:
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A;Residues: 1-289 - 12P>
A;Cross-references: UNIPROT:P23463
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                        Length 254;
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81.8%; Pred. No. 15;
:ive 0; Mismatches 2; Indels
                                                                                                                                                                                                 3; Indels
                                                                                                                                        Score 42; DB 2;
Pred. No. 13;
                                                                                                                                                                                               0; Mismatches
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Best Local Similarity 66.7%;
Matches 10; Conservative
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1 Similarity 70.6%;
12; Conservative
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homeotic protein Hox D8 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.0
''n 9; Conservative
                                                            A; Map position: 1
C; Superfamily: 14-3-3 protein
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                                                                                                                                          Query Match
Best Local Similarity
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C;Accession: E84764
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Wiesner, P.; Beck, J.; Beck, K.F.; Ripka, S.; Mueller, G.; Luecke, S.; Schweizer, E. Eur. J. Biochem. 177, 69-79, 1988
A;Title: Isolation and sequence analysis of the fatty acid synthetase FAS2 gene from Peni. A;Reference number: S01787; MUID:89030697; PMID:3053172
A;Accession: S01787
A;Accession: S01787
A;Accession: Compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT:082182; GB:AE002093; NID:93668094; PIDN:AAC61826.1; GSPDB:GN(
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A; Residues: 1-1857 <WIE>
A; Cross-references: UNIPROT: P15368; GB: M37461; NID: g169179; PIDN: AAA33695.1; PID: g169180
A; Note: the source is designated as Penicillium patulum
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C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T27431
A; Reference number: Z20365
A; Accession: T27431
A; Status: preliminary; translated from GB/EMBL/DDBJ
hypothetical protein At2g35090 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Penicillium griseofulvum
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 9.7;
0; Mismatches
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C,Superfamily: yeast fatty-acid synthase
C,Keywords: acyltransferase; coenzyme A
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14:05:32

31

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182 KAAKYAAFAARKKAAAVAA 200
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A,Map position: circular chromosome
C,Superfamily: formate dehydrogenase
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Best Local Similarity 61.5%;
Matches 8; Conservative
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343 AAEFEAYRAAVDA 355
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Best Local Similarity 61.5
Matches 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-788 <KUR>
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T13690
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GNVVSR
genome polyprotein 1 - tomato ringspot virus (strain raspberry) (fragment)
C; Species: tomato ringspot virus
C; Sepe-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C; Accession: A40787
R; Rott, M.E.; Tremaine, J.H.; Rochon, D.M.
Virology 185, 468-472, 1991
A; Reference number: A40787; MUD:92024112; PMID:1926788
A; Reference number: A40787; MUD:92024112; PMID:1926788
A; Reference number: A40787
A; Molecule type: genomic RNA
A; Residues: 1-354 <ROT>
A; Residues: 1-354 <ROT>
A; Residues: 1-354 <ROT>
A; Residues: 1-354 <ROT>
A; Map position: segment 1
C; Superfamily: tomato ringspot virus genome polyprotein
C; Seywords: glycoprotein; polyprotein
C; Keywords: glycoprotein; polyprotein
C; Keywords: glycoprotein; polyprotein
F; 270/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cidate: 17-301-1998 #sequence_revision 17-301-1998 #text_change 16-Aug-2004
Cidate: Sars, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: C70521
A;Accession: C70521
A;Accession: C70521
A;Accession: C70521
A;Catus: preliminary; nucleic acid sequence not shown; translation not shown
A;Bediques: 1-251 acOL
A;Coss-references: UNIPROT:007808; GB:Z97188; GB:AL123456; NID:g3261805; PIDN:CAB10008.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3815c
C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase
C;Keywords: acyltransferase; coenzyme A
A;Residues: 1-2129 <WIL>
A;Cross-references: UNIPROT:Q9U1R8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP:YA;Experimental source: clone Y79H2A
C;Genetics:
A;Gene: CESP:Y79H2A.3
A;Introns: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1; 67; 1760/1; 1929/3; 2037/3; 2074/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) homolog - Mycobacterium tuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 251;
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Pred. No. 1.4e+02;
2; Mismatches 2; Indels
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229 EAARMEADEAAARAA 243
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Best Local Similarity 66.7%;
Matches 8; Conservative
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144 EYAKYERYRSAA 155
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probable oxidoreductase (PA5181) [imported] - Agrobacterium tumefaciens (strain C58, Cer C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: F97547
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPROT: Q8UF51; GB: AE007869; PIDN: AAK87335.1; PID: 915156635; GSPDB: G
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Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cipate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
Cipate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
Cipate: 11-Jan-2002
RiWood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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Pred. No. 80;
3; Mismatches
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completed: March 31, 2005, 02:42:27 te : 19.9032 secs
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T18535
high molecular mass nuclear antigen - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18535
R;Shimada, K.; Harata, M.; Mizuno, S.
J. Cell Sci. 110, 3031-3041, 1997
A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick A;Reference number: Z18955; MUID:9803440; PMID:9365273
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G75512
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: G75512
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID: 20036896; PMID: 10567266
                                                                                                                                                                                                                                                                               A, Residues: 1-806 <MUR>
A, Cross-references: UNIPROT:096828; EMBL:AL031863; NID:e1331652; PID:e1355938; PIDN:CAA2
C, Genetics:
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A;Molecule type: mRNA
A;Residues: 1-1151 <SHI>
A;Cross-references: UNIPROT:057580; EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA241
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A;Molecule type: DNA
A;Residues: 1-101 <WHI>
A;Cross-references: UNIPROT:Q9RX23; GB:AE001908; GB:AE000513; NID:g6458174; PIDN:AAF1006
A;Experimental source: strain R1
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C; Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C; Accession: T13690
R; Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A; Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A; Reference number: Z17699
A; Accession: T13690
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2; Length 806;
Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: FlyBase:FBgn0025833
A;Introns: 37/3; 448/3; 611/2; 690/3
A;Note: EG:EG0003.2
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69.2%;
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Best Local Similarity 69.2%
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A;Gene: DR0492
A;Map position:
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C; Accession: E81312
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanvliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A; Reference number: A81250; MUID: 20150912; PMID: 10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:09PNK4; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7334!
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                         probable lipoprotein Cj1090c [imported] - Campylobacter jejuni (strain NCTC 11168)
C, Species: Campylobacter jejuni
C, Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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  Score 39; DB 2; Length 101; Pred. No. 17; 3; Indels 4; Mismatches
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h 55.7%;
Similarity 50.0%;
7; Conservative
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137 DSARYEAIRAASSEA 151
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70 DSAHYQAYRAKAGA 83
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Matches 7; Conservative
Query Match
Best Local Similarity
Matches 7; Conserv
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A;Residues: 1-170 <PAR>
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A; Status: preliminary
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds
 (without alignments)
95.342 Million cell updates/sec Run on:

1 EAAKYEAYKAAAAA 15 US-10-056-583A-64 70 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q7sc23 neurospora						Q64jv3 plasmodium						plasmo	aedes	aedes	Q6dlt9 aedes albop		plasmo			desulf	erwini	_	Q87sy7 vibrio para	arabi		P23463 mus musculu	1 homo	P13378 homo sapien	oryza	Q8w0dl oryza sativ
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Q615H3 SERA_ARCFU Q64JV6 Q94JV6 Q045G37 Q076G37 Q082182 Q95V10 Q67WS1 Q61KS8 Q6AV91 Q6QUT5	Q6i5h3 oryza sativ Q29445 archaeoglob		Q9ndj0 plasmodium	Q64jw6 plasmodium		P80676 blaberus cr		Q95v10 fasciola he		Q8irs8 drosophila		-	Q7xvb8 oryza sativ
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							41	41	41	41	41	41	41

ALIGNMENTS

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RN [1]
SEQUENCE FROM N.A.

RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

A Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

RA Dui D., Ianakiev P., Pedersen D., Nelsen C.B., Butler J., Endrizzi M.,

RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

RA Schitzennikoff C.P., Kinsey J.A., Barrett R., Greenberg D.,

RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;

"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 0:0-0(2003).
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                                                                                                                                                                        Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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847 AA; 94963 MW; CDAF7CSDSEFD910A CRC64;
                                                                                Created)
Last sequence update)
Last annotation update)
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66.7%; Pred. No. 56;
iive 1; Mismatches
                                          847 AA
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EMBL/GenBank, ...

EMBL; AABX01000143; EAA34000.1; -.

InterPro; IPR004648; Oligpept_transpt.

ThterPro; IPR004813; Tetrpept_transpt.

TherPro; IPR004813; Tetrpept_transpt.
                                          PRT;
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                                                                             01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 66.7
Matches 10, Conservative
                                        PRELIMINARY;
                                                                                                                                              Hypothetical protein.
Name=NCU08397.1;
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RESULT 1
Q7SC23
ID Q7SC23
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DAAKYEAYSPAYLAA 476 1 EAAKYEAYKAAAAA 15 462 g ઠે

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RESULT

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"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004).
EMBL; AY454085; AAS10471.1; -.
                                                                                                                                                                                                                                           PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
Plasmodium vivax.
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                  NCBI_TaxID=5855;
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EMBL; AY454088; AAS10474.1; -.
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EMBL; AY454087; AAS10473.1; -.
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Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                     Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
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603 603
603 AA; 65111 MW; 9FB464A42ED295C4 CRC64;
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608 608
608 AA, 65834 MW, FEC7E2627E333604 CRC64;
                         064JV8
064JV8;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
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Q64JW1;
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264JV9
ID 264JV9
AC 264J
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Q64JW1
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EMBL; AY454094; AAS10480.1; -.
                                                                                                                                                                                                                                                                            STRAIN=Ong;
PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
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25-OCT-2004 (TrEMBLrel. 28,
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SEQUENCE FROM N.A.
       NCBI_TaxID=5855;
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EMBL; AY454098; AAS10484.1; -.
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                                                                                                                                    STRAIN=Thai;
PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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Barnwell J.W.;
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                      Plasmodium vivax.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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78545 MW; EAD28262EF32531B CRC64;
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727 AA; 78556 MW; B3A309A6874F5B0D CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
Plasmodium vivax.
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Merozoite surface protein 3b (Fragment).
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Best Local Similarity 78.6
Matches 11; Conservative
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727 AA;
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Matches 11; Conserv
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Q644V3
ID Q644
AC Q644
AC Q644
DT 25-0
DT 25-0
DE Mero
OS Plags
OC Buka
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Q64JV7
ID Q64J
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"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004).

EMBL; AY454089; AAS10475.1; -.
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EMBL; AY454092; AAS10478.1; -.
PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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NCBI_TaxID=5855;
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NCBI_TaxID=5855;
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727 AA; 78668 MW; P1D764F1BB782E5C CRC64;
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810 810
810 AA; 86539 MW; 14B1E39FAE44F74A CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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EMBL; AY454081; AAS10467.1; -.
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Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
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                                               "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004).

EMBL; AY454083; AAS10469.1; -.
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Barnwell J.W.;
                     Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R., Barnwell J.W.;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5855;
                                                                                                                                                                                                                                                                                                                                                                       Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 64.3%; Score 45; DB 2; Length 897; Best Local Similarity 78.6%; Pred. No. 86; Matches 11; Conservative 0; Mismatches 3; Indels
                                                                                                                                                    Score 45; DB 2; Length 826;
Pred. No. 80;
                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  897 897
897 AA, 96705 MW, CB86EFCD3CBED5EA CRC64;
                                                                                                                 826 82, 826 AM; 699BIF21F5B747B6 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                             0; Mismatches
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Best Local Similarity 78.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                              572 EAAKEEAQKAATAA 585
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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               PubMed=15374528;
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SEQUENCE
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                                                                                                                          SEQUENCE
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Q64JW4
ID Q64JW
AC Q64JW
AC 25-OC DT 25-OC DT 25-OC DE ENAR OX NCBI
RN (1)
RP SEQUE
RC STRAIE
RX PUDME
RA RAYDE
RA BAINW
RT "Plas
                                                                                                                                                                                                                                                                   RESULT 11
Q64JW5
ID Q64JW
AC 264JW
AC 25-OC
DT 25-OC
DT 25-OC
DE METOZ
OX NCBI
RN (1)
RN (1)
RR RAYDE
RA BATDW
RT POIYT
RY POIYT
RY METOZ
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Gaps
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EMBL; AY454095; AAS10481.1; -.
                                                                                                                                                                                                                                                                  Gaps
polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004).
EMBL; AY454082; AAS10468.1; -.
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Barnwell J.W.;
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Aedes.
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                                                                                                                                                                                                   Score 45; DB 2; Length 900;
Pred. No. 86;
0; Mismatches 3; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY663380; AAT69676.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005261; F:cation channel activity; IEA.
GO; GO:0006812; P:cation transport; IEA.
InterPro; IPR005821; Ion_trans.
InterPro; IPR005820; M+channel_nlg.
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927 927
927 AA; 99734 MW; B5DCBD6130A7F4E1 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Voltage-dependent para-like sodium channel (Fragment).
                                                                                                                          900 900
900 AA; 97231 MW; DC84487C0D34BF7B CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 AA
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78.6%;
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Best Local Similarity 78.6
Matches 11; Conservative
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Voltage-dependent para-like sodium channel (Fragment).
Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NCEL TaxID=7160;
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY663381; AAT69677.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005261; F:cation channel activity; IEA.
GO; GO:0006812; P:cation transport; IEA.
InterPro; IPR005821; Ion trans.
InterPro; IPR005821; Ion trans.
InterPro; IPR00580; M+channel_nlg.
Pfam; PF00520; Ion trans; 2.
Ion transport; Ionic channel; Transmembrane; Transport.
NON_TER
                                                                                                                                                                                                                                                            Query Match 62.9%; Score 44; DB 2; Length 501; Best Local Similarity 73.3%; Pred. No. 73; Matches 11; Conservative 1; Mismatches 3; Indels
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Pfam; PF00520; Ion_trans; 2.
Ion transport; Ionic channel; Transmembrane; Transport.
NON_TER 1 1 1 1 1 1 NON_TER 501 501 S01 SEQUENCE 501 AA; 56497 MW; B66CD123B5EC5FDD CRC64;
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76 KAAKLEAQAAAAAA 90
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SEQUENCE
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QEDLT7;
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Q6DLT7
ID Q6DLT7
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Db . 76 KÄÄKLEÄQAÄÄÄÄÄ 90 Search completed: March 31, 2005, 02:41:07 Job time : 82.5645 secs

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5.1.6 Compugen Ltd. version : GenCore Copyright (c) 1993

- protein search, using sw model OM protein

March 31, 2005, 02:17:12 ; Search time 100.629 Seconds (without alignments) 65.338 Million cell updates/sec Run on:

US-10-056-583A-88 82

1 APEKAKYEAYKAAAAA 17 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

0B 0B Minimum Maximum

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp1980s:*

geneseqp2003as:*geneseqp2003bs:* geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

2 0	Description	Abp52294 HLA-DR2 m	5 HLA-DR2	3 HLA-DR2	Abp52271 HLA-DR2 m	_	HLA-DR2	Abp52302 HLA-DR2 m	Abp52270 HLA-DR2 m	HLA-DR2	HLA-DR2	OR2	Abp52272 HLA-DR2 m	Abp52259 HLA-DR2 m	HLA-	HLA-DR2	HLA-DR2	Abp52251 HLA-DR2 m	Abp52239 HLA-DR2 m	HLA-DR2	Abp52261 HLA-DR2 m	Abp52244 HLA-DR2 m		Abp52269 HLA-DR2 m	-DR2	HLA-
SOMMAKIES	ID	ABP52294	ABP52295	ABP52303	ABP52271	ABP52298	ABP52296	ABP52302	ABP52270	ABP52301	ABP52291	ABP52263	ABP52272	ABP52259	ABP52257	ABP52297	ABP52253	ABP52251	ABP52239	ABP52290	ABP52261	ABP52244	ABP52292	ABP52269	ABP52262	ABP52264
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4 4 6 5 3 3 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22226626666666666666666666666666666666	44 45 45

ALIGNMENTS

HLA-DR2 molecule binding peptide SEQ ID NO:88. ABP52294 standard; peptide; 17 AA. (first entry) 16-OCT-2002 ABP52294; RESULT 1 ABP52294

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens Synthetic. Ношо

WO200259143-A2.

01-AUG-2002.

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE.

Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

a major treating a New compositions comprising synthetic peptides in complex with histocompatibility complex class II HLADR2 protein, useful for demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

Sequence 19 AA;

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine CC residues. The complex of the peptide with a major histocompatibility CC residues. The complex of the peptide with a major histocompatibility an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine compressing condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention
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such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                 100.0%; Score 82; DB 5; Length 17; 100.0%; Pred. No. 1.6e-06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP52295 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fridkis-Hareli
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encephalomyelitis.
                                                                                                                                                                                                                                                 Sequence 17 AA;
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                                                                                                                                                                             invention
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Score 82; DB 5; Length 19; Pred. No. 1.8e-06;
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                                 Indels
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                                  0; Mismatches
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 100.08;
                                                                   1 APEKAKYEAYKAAAAA 17
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                   100.08;
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                                 17; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
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Matches
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HLA-DR2 molecule binding peptide SEQ ID NO:65.
    ABP52271 standard; peptide; 15 AA.
            (first entry)
            16-OCT-2002
        ABPS2271;
RESULT
  ABP522
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens Synthetic Homo

WO200259143-A2

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Fridkis-Hareli M; Strominger JL,

WPI; 2002-608439/65.

ಹ New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to invention

Sequence 15 AA;

Gaps ; 0 Score 71; DB 5; Length 15; Pred. No. 8.8e-05;); Mismatches 0; Indels 86.6%; Scc... 100.0%; Pre Query Match
Best Local Similarity 100...

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EKAKYEAYKAAAAAA 15

RESULT 5 ABP52298 ID ABP5

ABP52298 standard; peptide; 15 AA.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; HLA-DR2 molecule binding peptide SEQ ID NO:92. anti-tumour necrosis factor agent 16-OCT-2002 (first entry) ABP52298

sapiens. Synthetic. Homo

WO200259143-A2

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

a major treating a New compositions comprising synthetic peptides in complex with histocompatibility complex class II HLADR2 protein, useful for demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to invention

Sequence 15 AA;

Gaps ö Length 15; Indels DB 5; Lel . 8.8e-05; ches 0; Score 71; DB : Pred. No. 8.8 0; Mismatches 86.0 100.0%; Fr 86.68; Query Match Best Local Similarity 100. Matches 15; Conservative

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17 3 EKAKYEAYKAAAAA

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15 EKAKYEAYKAAAAA

ABP52296 standard; peptide; 17 AA. ABP52296; ABP52296
1D ABP5
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AC ABP5
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DT 16-0
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DE HLAXX

RESULT 6

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16-OCT-2002 (first entry)

HLA-DR2 molecule binding peptide SEQ ID NO:90.

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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100.08; Pre-
                                                                                       anti-tumour necrosis factor agent
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Best Local Similarity 100.
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                                                                                                                         Homo sapiens.
Synthetic.
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinations diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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Pred. No. 0.00021;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Page 39; 54pp; English.
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Homo sapiens.
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                                                                                                                            New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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                                                                          Strominger JL, Fridkis-Hareli
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24-JAN-2002; 2002WO-US002071.
                        24-JAN-2001; 2001US-0263569P
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                                                                                                   WPI; 2002-608439/65
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                                                    New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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Pred. No. 0.0018;
;; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                Claim 28; Page 39; 54pp; English.
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1 EKAKFEAFKAAAAA 15
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Best Local Similarity 86.7
Matches 13; Conservative
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WPI; 2002-608439/65.
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AC ABPP
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DT 16-0
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                                                          with an amino acid sequence with tynosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                compositions (I) comprising a peptide
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Pred. No. 0.0039;
0; Mismatches 2; Indels
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                Claim 28; Page 39; 54pp; English
                                              present invention describes
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                     Sequence 15 AA;
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ID ABP5
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AC ABP6
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DE HLA-
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KW HLA-
KW HLA-
KW HLA-
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KW HLA-
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New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral

WPI; 2002-608439/65

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

Example 1; Page 33; 54pp; English.

encephalomyelitis.

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immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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Pred. No. 0.0039;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP52272 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                       74.4%;
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                          invention
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ABP52305 represent peptides used in the exemplification of the present invention
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Pred. No. 0.0057;
); Mismatches 2; Indels
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                                                                                                                                                                  73.2%;
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Matches 13; Conserv
                                                                                                 Sequence 15 AA;
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ABP52259
ID ABP52259
XX ABP52259
XX ABP52
XX HUMAN
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Score 59; DB 5; Length 15; Pred. No. 0.0083;

72.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
                                                                                                                                                                                                                                                                    Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
Gaps
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Indels
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5
                                                                                                                                                                                                                                      HLA-DR2 molecule binding peptide SEQ ID NO:51.
Mismatches
                                                                                                                                                                                                                                                                                                                                                     anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 32; 54pp; English.
                                                                                                                                        ABP52257 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fridkis-Hareli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2002; 2002WO-US002071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2001; 2001US-0263569P
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                                                                                                                                                                                                       16-OCT-2002 (first entry)
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13; Conservative
                             EKAKYEAYKAAAAA
                                                           1 EKAAYAAYKAAAAA
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hes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-608439/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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Matches
Matches
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                       Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.5%; Score 57; DB 5; Length 15; 80.0%; Pred. No. 0.018; 2; Indels iive
                                                                                                                                                  HLA-DR2 molecule binding peptide SEQ ID NO:91.
                                     ABP52297 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; Page 39; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2002; 2002WO-US002071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2001; 2001US-0263569P.
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-608439/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                  WO200259143-A2.
                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                16-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-2002
                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                          ABP52297;
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RESULT 15
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Search completed: March 31, 2005, 02:35:27 Job time : 100.629 secs EKPKFEAYKAAAPA 15 g

3 EKAKYEAYKAAAAA 17

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Best Local Similarity 80.0 Matches 12; Conservative

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Gaps

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us-10-056-583a-88.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 31, 2005, 02:26:53; Search time 26.0484 Seconds (without alignments)
48.718 Million cell updates/sec Run on:

US-10-056-583A-88 82

1 APEKAKYEAYKAAAAA 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

513545 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*
.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		a p (
Result No.	Score	Query Match	Length	DB	OI	Description
-	44	53.7	596	2	US-08-836-620A-16	Sequence 16, Appl
7	43	52.4	162	4	US-09-732-210-1445	1445
m	43	52.4	324	4	US-09-248-796A-17156	17156,
4	42	51.2	13	Ŋ	PCT-US95-04121-38	38,
വ	42	Н	190	4	US-09-902-540-14713	147]
9	42	51.2	273	4	US-09-910-430-34	
7	42	51.2	1001	4	US-09-248-796A-18658	186
80	41	50.0	402	4	US-09-248-796A-17859	Sequence 17859, A
σ	40	48.8	13	ഗ	PCT-US94-10257A-33	33,
10	40	48.8	26	4	US-09-405-743A-3	Sequence 3, Appli
11	40	48.8	26	4	US-09-816-989A-3	'n
12	40	48.8	77	4	US-09-405-743A-5	Ŋ
13	40	48.8	77	4	US-09-816-989A-5	Ŋ
14	40	48.8	98	4	US-09-405-743A-6	9
15	40	48.8	98	4	US-09-816-989A-6	9
16	40	48.8	109	4	US-09-405-743A-7	7
17	40	48.8	109	4	US-09-816-989A-7	Sequence 7, Appli
18	40	48.8	466	4	US-09-489-039A-13950	139
19	40	48.8	802	4	US-09-489-039A-11230	Sequence 11230, A
	40	•	1156	4	-09	171
	40	48.8	1562	4	US-09-438-185A-152	15
	39	47.6	38	m	US-09-117-121-16	16,
		47.6	38	ო	US-09-117-121-24	24,
24	39	47.6	38	4	US-09-344-529-5	5, 7
		•	166	4	-09-252-991A	Sequence 22139, A
26	39	47.6	202	4	-09-205-	
27	39	47.6	219	4	US-09-902-540-16623	16623

Sequence 6391, Ap	Sequence 18456, A	Sequence 6, Appli	Sequence 6, Appli	4	218	Seguence 18769, A	Sequence 5116, Ap			Sequence 2, Appli		1124	Sequence 45793, A	Sequence 652, App	615,	7442,	
US-09-107-532A-6391	US-09-248-796A-18456	US-08-295-670-6	US-08-633-485-6	US-08-508-761B-4	US-09-252-991A-21824	US-09-252-991A-18769	US-09-543-681A-5116	US-09-117-121-30	US-08-245-511-2	US-08-600-993A-2	US-10-144-198-28	US-09-902-540-11242	US-09-270-767-45793	US-09-198-452A-652	US-09-438-185A-615	US-09-489-039A-7442	US-09-328-352-4861
4	4	Н		ო	4	4	4	m	~	7	4	4	4	4	4	4	4
309	411	497	497	510	601	731	459	24	163	163	171	186	319	333	335	351	391
47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.0	46.3	46.3	46.3	46.3	46.3	46.3	46.3	46.3	46.3	46.3
39	39	39	39	39	39	39	38.5	38	38	38	38	38	38	38	38	38	38
28	29	30	31	32	33	34	35		37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Length 596;
                                                                                                                                                                                            TITELON: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.7%; Score 44; DB 2; Best Local Similarity 68.8%; Pred. No. 28; Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION NUMBER: US/08/836,620A
FILING DATE:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
PRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
                                                              Sequence 16, Application US/08836620A; Patent No. 5958710; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 596 amino acide TYPE: amino acid
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ORGANISM: Ra
RESULT 1
US-08-836-620A-16
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Gaps

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Indels

RESULT 2 US-09-732-210-1445

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Sequence 14713, Application US/09902540

| Sequence 14713, Application US/09902540
| Patent No. 6833447
| GENERAL INFORMATION:
| APPLICANT: Goldman, Barry S.
| APPLICANT: Hinkle, Gregory J.
| APPLICANT: Slater, Steven C.
| APPLICANT: Wiegand, Roger C.
| TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
| CURRENT APPLICATION NUMBER: US/09/902,540
| CURRENT FILING DATE: 2000-07-10
| PRIOR FILING DATE: 2000-07-10
| NUMBER OF SEQ ID NOS: 16825
| SEQ ID NO 14713
| LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 5; Length 13; Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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                      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04121
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,206
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                      NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 079.2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6010
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Sequence 34, Application US/09910430
// Patent No. 6794166
// GENERAL INFORMATION:
// APPLICANT: Godfroi, Edmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||: :| ::|||
120 APERTEYRVWRAAA 133
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                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
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1 AAYKAAKAAAAA 13
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Best Local Similarity 76.9
Matches 10; Conservative
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Matches 7; Conservative
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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US-09-902-540-14713
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US-09-248-796A-17156

Sequence 17156, Application US/09248796A

Sequence 17156, Application US/09248796A

Sequence 17156, Application US/09248796A

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

FRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
           Patent No. 6573361

; Patent No. 6573361

; APPLICANT: Bunkers, Greg J.

APPLICANT: Liang, Jihong

APPLICANT: Liang, Jihong

APPLICANT: Mittanck, Cindy A.

APPLICANT: Mittanck, Cindy A.

APPLICANT: Seale, Jeffrey W.

APPLICANT: Mu, Yonnie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use

FILE REFERENCE: 38-21(15036)B

CURRENT APPLICATION NUMBER: US 60/169,513

PRIOR APPLICATION NUMBER: US 60/169,513

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 1445

LENGTH: 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.4%; Score 43; DB 4; Length 162; 52.9%; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
NUMBER OF SEQUENCES: 62
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mycobacterium tuberculosis US-09-732-210-1445
Sequence 1445, Application US/09732210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APEKAKYEAYKAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.4%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 APEKAKEESAPAA 170
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; ORGANISM: Candida albicans
US-09-248-796A-17156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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APPLICANT: BRIGITTE DEVAUX
APPLICANT: JONATHAN B. ROTHBARD
APPLICANT: DAWN SMILEK
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                        Length 402;
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                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                           Score 41; DB 4
Pred. No. 57;
1; Mismatches
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0; Mismatches
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17859
LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10257A
FILING DATE: 1 SEPTEMBER 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ANNE I CRAIG
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 071.1 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application PC/TUS9410257A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,824
FILING DATE: 03-SEP-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.8%;
                                                                                                                                                                                                                                                           50.0%;
80.0%;
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                                                                                                                                                                             TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: .13 amino acids
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                8; Conservative
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC
                                                                                                                                                                                                                                                                                                                                                                 |||||:| ||
70 KAKYESYDAA 79
                                                                                                                                                                                                                                                                                                                                         4 KAKYEAYKAA 13
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Best Local Similarity
Matches 8; Conserv
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PILING DATE: 1999-02-12
PRIOR PILING DATE: 1999-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18658
LENGTH: 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . LOCATION: (21)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-18658
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
 ## APPLICANT: Leboulle, Gerard

TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACERIZATION OF

TITLE OF INVENTION: EXPRESSED IN THE IXODES RICINUS SALIVARY

TITLE OF INVENTION: GLANDS

FILE REFERENCE: VANM229.001CP1

CURRENT APPLICATION NUMBER: US/09/910,430

CURRENT FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: PCT/BE00/00061

PRIOR APPLICATION NUMBER: GB 9913425.6

PRIOR PILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 34

LENGTH: 273
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
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Pred. No.
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Patent No. 6747137
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Similarity 52.9%;
9; Conservative 1
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Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Ixodes ricinus
US-09-910-430-34
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-248-796A-18658
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
FILE REFERENCE: 2609/60807-A-PCT-US
FILE REFERENCE: 2001-03-23
FRIOR APPLICATION NUMBER: G0/101,693
FRIOR APPLICATION NUMBER: PCT/US99/22402
FRIOR PILING DATE: 1998-09-25
FRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 77
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Sequence 6, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Description of Artificial Sequence: CTHER INFORMATION: PEPTIDE US-09-405-743A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09816989A Patent No. 6800287 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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18 AAKKAEAKAYKAAEA 32
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18 AAKKAEAKAYKAAEA 32
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US-09-816-989A-5
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US-09-405-743A-6
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; Sequence 3, Application US/09816989A
; Sequence 3, Application US/09816989A
; Sequence 3, Application US/0287
; GENERAL INFORMATION:
    APPLICANT: Gad, Alexander
    APPLICANT: Lis, Doris
    TITLE OF INVENTION: AND FOR THERAPEUTIC USE
    TITLE OF INVENTION: AND FOR THERAPEUTIC USE
    TITLE OF INVENTION NUMBER: US/09/816,989A
; CURRENT APPLICATION NUMBER: G0/101,693
    PRIOR FILING DATE: 1998-09-25
    PRIOR FILING DATE: 1998-09-25
    PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
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                                                                                                 US-09-405-743A-3

Sequence 3, Application US/09405743A

Patent No. 6514938

GENERAL INFORMATION:

APPLICANT: Yeda Research and Development Co., Ltd.

TITLE OF INVENTION:

FILE REFERENCE: 60807-A

CURRENT APPLICATION NUMBER: US/09/405,743A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 56

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: PEPTIDE
US-09-405-743A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
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18 AAKKAEAKAYKAAEA 32
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18 AAKKAEAKAYKAAEA 32
            1 AAYAAAKAAAAA 13
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US-09-816-989A-3
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US-09-405-743A-5
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Section 10. Sectio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-6
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ORGANISM: Artificial Sequence
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18 AAKKAEAKAYKAAEA 32
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18 AAKKAEAKAYKAAEA 32
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US-09-816-989A-6
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us-10-056-583a-88.rapb

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March 31, 2005, 02:29:23; Search time 75.4032 Seconds (without alignments) 74.648 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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82
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence	Semience											
	. QI	US-10-056-583-88	US-10-056-583-89	US-10-056-583-97	US-10-056-583-65	US-10-056-583-90	US-10-056-583-96	US-10-056-583-64	US-10-056-583-95	US-10-056-583-92	US-10-056-583-57	US-10-056-583-85	US-10-056-583-66	08-10-056-583-51
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ф	Query Match	100.0	100.0	89.0	96.6	96.6	84.1	79.3	76.8	75.6	74.4	74.4	73.2	72.0
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RESULT.2 US-10-056-583-89

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Publication No. US20030064915A1;
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: TONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
                                                                         APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT APPLICATION NUMBER: 60/263,569
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 82; DB 14; Length 19; Best Local Similarity 100.0%; Pred. No. 1.8e-06; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-89
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88.2%; Pred. No. 4.7e-05;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 89, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APEKAKYEAYKAAAAA 17
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Matches 15; Conservative
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APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
                                                                                                                                                                                                                                                                                                                                                                                                                        ), OTHER INFORMATION: The peptide was designed and synthesized US-10-056-581-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.6%; Score 71; DB 14; Length 15; 100.0%; Pred. No. 8.6e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
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APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Presidents and Fellows of Harvard College
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.6%; Score 71; DB 14; I
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 24655-017;
CURRENT APPLICATION NUMBER: US/10/056,583;
CURRENT FILING DATE: 2002-01-24;
PRIOR APPLICATION NUMBER: 60/263,569;
PRIOR FILING DATE: 2001-01-24;
NUMBER OF SEQ ID NOS: 99;
SOFTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 90;
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 96, Application US/10056583 Publication No. US20030064915A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 90, Application US/10056583 Publication No. US20030064915A1
                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EKAKYEAYKAAAAA 15
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Best Local Similarity 100.
Matches 15; Conservative
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us-10-056-583a-88.rapb

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TYPE: PRT ORGANISM: Artificial Sequence
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Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

TITLE OF INVENTION: 10002-01-24

PRIOR PPLICATION NUMBER: 60/263,569

PRIOR PPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 64
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GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
                                                                                                                                                                                                                                                                                                                                                           Query Match 84.1%; Score 69; DB 14; Length 17; Best Local Similarity 82.4%; Pred. No. 0.00021; Matches 14; Conservative 2; Mismatches 1; Indels
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CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 96
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application US/10056583 Publication No. US20030064915A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EKAKYEAYKAAAAA 17
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Best Local Similarity 93.37
Lhos 14; Conservative
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US-10-056-583-64
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Feduence 57, Application US/10056583

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

TITLE OF INVENTION: CONDITIONS

TITLE OF INVENTION: CONDITIONS

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT APPLICATION NUMBER: 60/263,569

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ'ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 57
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US-10-056-583-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-056-583-92; Sequence 92, Application US/10056583; Publication No. US20030064915A1; GENERAL INFORMATION: APPLICANT: Presidents and Fellows of Harvard College
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.8%; Score 63; DB 14; Best Local Similarity 86.7%; Pred. No. 0.0017; Matches 13; Conservative 2; Mismatches 0
                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 95
LENGTH: 15
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Pred. No. 0.0076;
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Pred. No. 0.0076;
           Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
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86.7%;
                                                     3 EKAKYEAYKAAAAA 17
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
           13; Conservative
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; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-57
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                                                                     Score 61; DB 14; Length 15; Pred. No. 0.0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.4%; Score 61; DB 14; Length 15; 86.7%; Pred. No. 0.0036; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 66, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Presidents and Fellows of Harvard College APPLICANT: Strominger, Jack L. APPLICANT: Fridkis-Hareli, Masha TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING TITLE OF INVENTION: CONDITIONS
                                                                                                           1; Mismatches
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CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                    Query Match 74.4%;
Best Local Similarity 86.7%;
Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
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LENGTH: 15
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Sequence 51, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 51

LENGTH: 15

LENGTH: 15

LENGTH: 15
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Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 53

LENGTH: 15
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CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
Indels
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RESULT 15
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Pridkis-Hartle Nasha
; TITLE OF INVENTION: THERAPETIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR PILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91
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Search completed: March 31, 2005, 02:48:48 Job time : 75.4032 secs

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0; Gaps

Query Match 69.5%; Score 57; DB 14; Length 15; Best Local Similarity 80.0%; Pred. No. 0.016; Matches 12; Conservative 1; Mismatches 2; Indels

3 EKAKYEAYKAAAAA 17

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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 31, 2005, 02:26:17; Search time 20.2903 Seconds (without alignments)
80.614 Million cell updates/sec Run on:

1 APEKAKYEAYKAAAAA 17 US-10-056-583A-88 82 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 · Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	45	54.9	154	7	H81076	conserved hypothet
8	45	54.9	154	7	B81866	
m	45	54.9	179	~	F97683	50S ribosomal prot
4	45	54.9	179	N	AF2908	ribosomal
ഹ	4.	54.3	189	~	S77930	keletal pr
9	44.5	54.3	189	~	877935	exoskeletal protei
7	44	53.7	599	Н	QRMSE	O
80	44	53.7	600	-	QRRTE	estrogen receptor
σ	43	52.4	162	7	H70927	
10	43	52.4	185	7	836290	T-cell receptor ga
11	43	52.4	347	N	A81794	m
	43	52.4	348	N	B81216	peptidyl-prolyl ci
13	43	52.4	421	0	JV0057	tolA protein - Esc
14	43	52.4	441	~	A43555	GAP-43-related pro
15	42	51.2	188	0	I50145	homeotic protein H
	42	51.2	289	0	A43562	homeotic protein H
17	42	51.2	329	~	D96030	hypothetical prote
18	42	51.2	1167	~	D97516	DNA polymerase III
19	42	51.2	1167	~	AD2735	DNA polymerase III
20	41	50.0	88	~	JC2184	transcription fact
21	41	50.0	129	-	TNLJG3	trans-activating t
22	41	50.0	177	0	AD1307	pept1dyl methionin
23	41	50.0	177	0	AD1679	
24	41	50.0	254	0	H86355	probable 14-3-3 pr
25	41	50.0	289	7	AC1399	
26	41	50.0	641	0	PH1919	FL-160-4 protein -
27	41	50.0	1885	-	JC4086	fatty-acid synthas
28	41	50.0	2129	7	T27431	Q.
29	40	48.8	73	7	S40015	phd protein - phag

M-like protein enn	trans-activating t	hypothetical prote	probable transcrip	probable fatty-aci	hypothetical prote	H+-transporting tw	conserved hypothet	hypothetical prote	hypothetical prote	translation initia	CT147 hypothetical	conserved hypothet	ct147 hypothetical	probable fatty-aci	fatty acid synthas
S61806	TNLJSZ	AB3271	A83492	T43037	AC2015	S04675	G70302	T50013	T13690	E64114	F86509	C81558	H72112	T43409	T38781
ο,	-	~	~	N	7	7	7	7	7	~	~	~	~	N	0
75	106	107	202	377	467	478	480	594	806	829	1537	1537	1537	1842	1842
48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8
40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40

ALIGNMENTS

	RESHET 1
	H81076
	conserved hypothetical protein NMB1500 [imported] - Neisseria meningitidis (strain MC58
_	C;Species: Neisseria meningitidis
	C;Date: 31-Mar-2000 #sequence revision 31-Mar-2000 #text change 09-Jul-2004
	C;Accession: H81076
	R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
	Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
	ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiqnani, V.; Pizza, M.
	Science 287, 1809-1815, 2000
_	A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
	A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
	A;Reference number: A81000; MUID:20175755; PMID:10710307
	A:Accession: H81076

A;Accession: H81076
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-154 <TET>
A;Cross-references: UNIPROT:Q9JYN4; GB:AE002499; GB:AE002098; NID:g7226737; PIDN:AAF4185
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1500
C;Superfamily: Escherichia coli ybdQ protein

Gaps . 0 Query Match 54.9%; Score 45; DB 2; Length 154; Best Local Similarity 56.2%; Pred. No. 5.4; Matches 9; Conservative 4; Mismatches 3; Indel8

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||| ::|:||| | 48 APEFLQHESYEAAAVA 63 1 APEKAKYEAYKAAAAA 16 g ઠ

Conserved hypothetical protein NWA1703 [imported] - Neisseria meningitidis (strain 22491 C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision:05-May-2000 #text_change 09-Jul-2004 C;Accession: B81866 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: B81866 A;Accession: B81866 A;Accession: Braiminary A;Molecule type: DNA A;Residues: 1-154 'c-PAR' A;Accession: L-154 'c-PAR' A;Residues: 1-154 'c-PAR' A;Coss-references: UNIPROT:Q9JTN1; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8493 A;Cross-references: UNIPROT:Q9JTN1; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8493 C;Genetics: A;Gene: NMA1703 C;Superfamily: Escherichia coli ybdQ protein

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9 AAEKARFFQAFKAAEAAA 26
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ilarity 61.1%;
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R.Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:d
A,Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                  C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97683
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPROT: Q8UBZ5; GB: AE007869; PIDN: AAK88423.1; PID: g15157917; GSPDB: d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C, Species: Agrobacterium tumefaciens C, Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C, Accession: AF2908
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A, Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A, Reference number: AB2577; MUID:21608550; PMID:11743193
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S4.9%; Score 45; DB 2; Length 179;

Best Local Similarity 64.7%; Pred. No. 6.3;

Matches 11; Conservative 1; Mismatches 5: Indele
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  Length 154;
                                                    3; Indels
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A;Gene: rplS
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Map position: circular chromosome
C, Superfamily: Escherichia coli ribosomal protein L19
Score 45; DB 2;
Pred. No. 5.4;
4; Mismatches
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                                                                                                           1 APEKAKYEAYKAAAA 16
    Query Match 54.9%;
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                          48 APEFLOHESYBAANA 63
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Matches 11; Conserv
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A; Status: preliminary
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exoskeletal protein HACP202A - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77930
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
Submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homarn
A;Reference number: S77925
A;Accession: S77930
A;Accession: S77930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 < NOU>
A;Cross-references: UNIPROT:Q7M496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exoskeletal protein HACP202B - American lobster (fragment)

C; Species: Homarus americanus (American lobster)

C; Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004

C; Accession: S77935

R; Nousiainen, M:; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.

Submitted to the Protein Sequence Database, June 1997

A; Description: Characterization of exoskeletal proteins from the American lobster, Homaru A; Reference number: S77925

A; Accession: S77935

A; Accession: S77935

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-189 < NOUS

A; Cross-references: UNIPROT: Q7M495
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A; Molecule type: MRNA
A; Residues: 1-599 <WHI>
A; Cross-references: UNIPROT: P19785; GB: M38651; NID: g193179; PIDN: AAA37580.1; PID: g193180
A; Cross-references: UNIPROT: P19785; GB: M38651; NID: g193179; PIDN: AAA37580.1; PID: g193180
C; Comment: The steroid hormones and their receptors are thought to be weakly &:
C; Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly &:
c; Superfamily: estrogen receptor; erbA transforming protein homology
C; Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptors; 1-183/Domain: amino-terminal <NH2>
F;1-183/Domain: amino-terminal ANH2>
F;184-275/Domain: bNA binding #status predicted <DNA>
F;187-460/Domain: erbA transforming protein homology <ERBA>
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c;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40061
R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A;Title: Structural organization and expression of the mouse estrogen receptor.
A;Reference number: A40061; MUID:91042558; PMID:2484714
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Pred. No. 8;
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T-cell receptor gamma chain precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36290; S23041
R;Hein, W.R.; Dudler, L.
EMBO J. 12, 715-724, 1993
A;Title: Divergent evolution of T cell repertoires: extensive diversity and developmenta A;Reference number: S36287; MUID:93178447; PMID:8440261
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R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81794
                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q10795; GB:Z74024; GB:AL,123456; NID:g3250700; PIDN:CAA98346.
A;Experimental source: strain H37Rv
C;Genetics:
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  A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70927
                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-162 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z12998; NID:g2260; PIDN:CAA78342.1; PID:g2261
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                  Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 2;
Pred. No. 25;
2; Mismatches
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3
                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 2
Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.4%; Score 43; 62.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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APKPSKLEVFNAALAAA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                     52.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APEKAKYEAYKAAAAA
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Best Local Similarity 62.59
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||| || || DKAKYSVYKGAA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EKAKYEAYKAAA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-185 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-347 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
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A; Residues: 1-487, 'T', 489-600 < MAG>
A; Cross-references: EMBL:X61098; NID:956120; PIDN:CAA43411.1; PID:956121
C; Comment: The steroid hormones and their receptors are involved in the regulation of eu C; Comment: In the absence of ligand, steroid hormone receptors appears to recognize discrete DNA sequences uperfream of transcriptional start sit c; Superfamily: estrogen receptor; erbA transforming protein homology
C; Keywords: DNA binding; steroid binding; steroid hormone recepts; 188-246 Domain: amino-terminal < NNA2>
F; 188-246 Domain: erbA transforming protein homology < ERBA>
F; 188-246 Domain: erbA transforming protein homology < ERBA>
F; 188-246 Fkegion: zinc finger CCCC motif F; 261-256 Kkegion: nuclear location signal F; 305-557 Domain: steroid binding #status predicted < STB>
F; 190, 193, 207, 210/Binding site: zinc (Cys) #status predicted
F; 226, 232, 245/Binding site: zinc (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: S07379; S16731
R;Koike, S.; Sakai, M.; Muramatsu, M.
Nucleic Acids Res. 15, 2499-2513, 1987
A;Title: Molecular cloning and characterization of rat estrogen receptor cDNA.
A;Reference number: S07379; MuID:87174780; PMID:3031601
A;Accession: S07379
A;Molecule type: mRNA
A;Residues: 1-600 <KOI>A;Accoss-references: UNIPROT:P06211; EMBL:Y00102; NID:g56110; PIDN:CAA68287.1; PID:g56111
R;Maggi, A.M.A.
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70927
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, SRajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                        Gaps
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F;187-210/Region: zinc finger CCCC motin
F;223-245/Region: zinc finger CCCC motin
F;260-275/Region: nuclear location signal
F;304-556/Domain: steroid binding #status predicted <STB>
F;189,192,206,209/Binding site: zinc (Cys) #status predicted
F;225,231,241,244/Binding site: zinc (Cys) #status predicted
F;240,309/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                     Score 44; DB 1; Length 599;
Pred. No. 30;
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Pred. No. 30;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                              53.7%; Scc.
68.8%; Pred
0; M
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68.8%;
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 68.8
Matches 11; Conservative
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A; Accession: $16731
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Best Local
Matches 1
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Gaps

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Indels

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C;Accession: A43555; S65398
R;Ng, S.C.; Perkins, L.A.; Conboy, G.; Perrimon, N.; Fishman, M.C.
Development 105, 629-638, 1989
A;Title: A Drosophila gene expressed in the embryonic CNS shares one conserved domain wit A;Reference number: A43555; MUID:90126372; PMID:2693037
A;Recession: A43555
A;Molecule type: mRNA
A;Residues: 1-441 «NGA»
A;Residues: 1-444 «NGA»
A;Cross-references: UNIPROT:P29746; EMBL:X63828
R;Perkins, L.A.
submitted to the EMBL Data Library, December 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: S65398
A;Accession: S65398
A;Molecule type: mRNA
A;Residues: 1-111,'AIPEKKTL',120,'EEAK',125,'AQENA',131,'VEAEKKQEKTARTE',146,'EPTVEAQP',1
A;Cross-references: EMBL:X63828; NID:97663; PID:97664
A;Note: the differences in residues 112-178 are due to frameshift errors
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C; Species: Gallus gallus (chicken)
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C; Accession: IS0145; S14512
B; Crompton, MR.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
A; Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic virus A; Reference number: IS0145; MUID:91238215; PMID:1674560
A; Accession: IS0145
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A;Molecule type: mRNA
A;Residues: 1-188 <CRO>
A;Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g62701
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Drosophila melanogaster
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;96-152/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 2; Length 441;
Pred. No. 32;
2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                     GAP-43-related protein - fruit fly (Drosophila melanogaster)
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Pred. No. 20;
0; Mismatches
        Pred. No. 30;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: FlyBase:FBgn0001090
A;Map position: 10
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     Similarity 73.3%;
11; Conservative (
                                                                                                                                                                                    215 AAEKAKAEAEKKAAA 229
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Best Local Similarity 58.8%;
Matches 10; Conservative
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illarity 81.8%;
Conservative
                                                                                                                 1 APEKAKYEAYKAAAA
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les 9; Conserv
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Best Local S
Matches 9
           Local
        Best Loc
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                                                                                                                                                                                                     peptidyl-prolyl cis-trans isomerase NMB0281 [imported] - Neisseria meningitidis (strain C; Species: Neisseria meningitidis C; Species: Neisseria meningitidis (cis-trans isomerase NMB0281 [imported] - Neisseria meningitidis (cis-trans cis-trans cis-transcord cis-transcord cis-transcord 
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JV0057
tolA protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produ A;Reference number: JV0057; MUID:90078104; PMID:2687247
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A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0281
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-421 < BLAT>
A; Cross-references: GB: AE000177; GB: U00096; NID: g1786955; PIDN: AAC73833.1; PID: g1786960; A; Experimental source: strain K-12, substrain MG1655
C; Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: nucleotide binding; P-loop; transmembrane protein F;14-34/Domain: transmembrane #status predicted <MSS>F;78-301/Domain: helical #status predicted <HSR>F;355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2;
Pred. No. 25;
2; Mismatches
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62.5%;
||:||| : ||| || apokaktasakaa 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:||| : ||| || APQKAKTASAKAA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-348 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 17 min A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JV0057
A; Molecule type: DNA
                                        15
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                                     원
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Indels

Search completed: March 31, 2005, 02:42:28 Job time : 21.2903 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

March 31, 2005, 02:18:02; Search time 91.3065 Seconds (without alignments) 95.342 Million cell updates/sec Run on:

US-10-056-583A-88 82 1 APEKAKYEAYKAAAAA 17

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q96m46 homo sapien	uncul	Q9jtn1 neisseria m	Q9jyn4 neisseria m	Q8ubz5 agrobacteri	O9vfl4 drosophila	-		Q9v7u6 drosophila		Q7m496 homarus ame	Q6lan9 rattus norv	Q8p7p0 xanthomonas	_		Q8sxm8 drosophila		P06211 rattus norv	Q9w327 drosophila		_		P50887 drosophila	Q7s9p3 neurospora			Q9ng86 drosophila		Q9ng88 drosophila		
	ID	Q96M46	Q64CP3	Q9JTN1	Q9JYN4	RL19 AGRTS	Q9VFL4	Q75GC3	Q6D7F3	907706	Q7M495	Q7M496	Q6LAN9	Q8P7P0	069J37	Q8A8P1	Q8SXM8	ESR1 MOUSE	, ESR1_RAT	Q9W327	RS16_MYCBO	RS16_MYCTU	Q71WI3	RL22_DROME	Q7S9P3	Q9UAN1	O9N603	O9NG86	Q9NG87	Q9NG88	Q9NGB9	Q9NG90
	ength DB	570 2	•	154 2	•	•	300 2	375 2	395 2	463 2	189 2	• •	113 2	272 2	306 2	316 2	574 2	599 1	600 1	607 2	162 1	162 1	289 2	•		312 2	•		•	319 2	•	•
عد	Query Match Length	61.0	58.5	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.3	54.3	53.7	53.7	53.7	53.7	53.7		53.7	53.7	52.4	52.4	52.4	52.4	52.4	52.4	N	52.4	52.4	$^{\circ}$	52.4	52.4
	Score	50	48	45	45	45	45	45	45	45	44.5	44.5	44	44	44	44	44	44	44	44	43	43	43	43	43	43	43	43	43	43	43	43
1	NO.	7	7	m	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

TYTOOPPRITH	Q8byx1 mus musculu Q6x3f6 pseudomonas
Q89J65 Q9JSP0 Q9K186 Q8EHS3 Q83SA1 TOLA ECOLI BNB DROME Q6QUTS Q7SGF5 Q6CCF1	Q8BYX1 Q6X3F6
0000010100000	0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	226
	51.8 51.2
	42.5
2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	44 45

ALIGNMENTS

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InterPro; IPR006015; Usp.
InterPro; IPR006016; UspA
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Best Local Similarity 56.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMB1500; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
RL19_AGRT5
ID RL19_AGRT5
AC Q8UBZ5;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
DT 28-FEB-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                           Q9JYN4
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MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hallam S.J., Putnam N., Preston C.M., Detter J.C., Rokhsar D., Richardson P.M., DeLong E.F.; "Reverse methanogenesis: testing the hypothesis with environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%; Score 48; DB 2; Length 707; 70.6%; Pred. No. 43; 4; Indels tive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Putnam N., Detter J.C., Richardson P.M., Rokhsar D.;
Putnam N., Detter J.C., Richardson P.M., Rokhsar D.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY714833; AAU82834.1; -.
Hypothetical protein.
SEQUENCE 707 AA; 78670 WW; 104FE803EA51973D CRC64;
                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein NMA1703.
OrderedLocusNames=NMA1703;
                                                                                                                                                                              707 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0006950; P:response to stress; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
                                                                                                                                                                                                                              Created)
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                               Archaea; environmental samples.
NCBI_TaxID=286721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 643 AAEKLKSEAERAAAAA 659
                                                                                                                                                                           Q64CP3
Q64CP3;
25-OCT-2004 (TrEMBLrel. 28, Cr
25-OCT-2004 (TrEMBLrel. 28, La
25-OCT-2004 (TrEMBLrel. 28, La
Hypothetical protein.
ORFNames=GZID1_21;
uncultured archaeon GZfosID1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APEKAKYEAYKAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 305:1457-1462(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 404:502-506(2000).
EMBL, AL162756; CAB84931.1;
PIR; B81866; B81866.
HSSP; P44880; lJWV.
                                                                194 PEKVKYEAYRTLA 206
                    PEKAKYEAYKAAA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q9JTN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
Nelson K.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58."_{\it i}
                                                                                                                                                                                          Gaps
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                                                                                                                   Length 154;
                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00582; Usp; 1.
PRINTS; PR01438; UNVRSLSTRESS.
Complete proteome; Hypothetical protein.
SEQUENCE 154 AA; 16524 MW; CBAB524DF5221CAB CRC64;
                                                      | protein.
C9C4AFDDF521D064 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein NMB1500.
                                                                                                                                 Score 45; DB 2;
Pred. No. 30;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0006950; P:response to stress; IEA.
InterPro; IPR006015; Usp.
InterPro; IPR006016; UspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                    Complete proteome; Hypothetical SEQUENCE 154 AA; 16552 MW; C
Pfam; PF00582; Usp; 1.
PRINTS; PR01438; UNVRSLSTRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE002499; AAF41856.1; -
PIR; H81076; H81076.
                                                                                                                                     54.9%;
56.2%;
                                                                                                                                                                                                                                               1 APEKAKYEAYKAAAA 16
                                                                                                                                                                                                                                                                                                 48 APEFLOHESYBAAVA 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 287:1809-1815(2000)
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Created) Last sequence update) Last annotation update)

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Drosophila melanogaster (Fruit fly)
                                            01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
25-OCT-2004 (TrEMBLrel. 28,
CG14840-PA (AT18408p).
ORFNames=CG14840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the ribosomal protein L19P family.
                                                                                                                                                                                                                                                                                 MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chapman V., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21608551; PubMed=11743194; DOI=10.1126/Science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
50S ribosomal protein L19.
Name=rplS; OrderedLocusNames=Atu2703, AGR C 4900;
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBL_TaxID=176299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F3256BA44A5AD2D1 CRC64;
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INCELPYO; IPR001857; Ribosomal L19.
PEam; PF01245; Ribosomal L19; 1.
PRINTS; PR00061; RIBOSOMĀLL19.
ProDom; PD002979; Ribosomal L19; 1.
TIGRFAMS; TIGR01024; rplS bact; 1.
PROSITE; PS01015; RIBOSOMĀL L19; 1.
Complete proteome; Ribosomal protein.
SEQUENCE 179 AA; 19474 MW; F3256BA4
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PIR; F97683; F97683.
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RA MEDLINE-2019 50005; Pubmed-1073132; DOI-10.1126/SCIECHCG. 2875-5461.2185; Radame M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides D.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutcon G.C., Nogers Y.H., Blazej R.G., Change M., Pfeiffer B.D., Raddon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D., Raddon R.C., Baxter E.G., Helt G., Nalson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Péannkoch C., Baldwin D., Ballow R.M., Basul A., Basul B.P., Bhandari D., Bolhakov S., Ballokva D., Botchan M.R., Bouch J., Bakendari D., Bolhakov S., Borthan M.R., Bouch J., Botchan M.R., Bouch J., Editor B., Erchier P., Britis R.C., Busam D.A., Buller H., Cadieu B., Center A., Chadra I., Radeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Burtis R.C., Busam D.A., Buller H., Cadieu B., Center A., Chadra I., Radeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Burtis R.C., Evangelista C.C., Ferrac C., Gabrielian A., Gargen N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Gaun P., Harris M.L., Lastor B.B., Hostin D., Houston K.A., Havyey D., Heiman T.J., Hermandez J.R., Harris M.L., Lastor B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ling Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Markel B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A., Moy M., Murphy B., Murphy L., Marzy D.M., Nelson D.L., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Shen H., Shen H., Shen H., Shen H., Shen E.C., Siden F., Sarpel C., Singeon M., Strong R., Such B., Shre B.C., Siden F., Wassaman D.A., Wainsenbach J., Wall Shrinkow E., Woodagorf, Worles R., Wang C.Y., Wassaman D.A., Wainsenbach J., Wall Shrinkow E., Sheng K.H., Wassaman D.A., Wainsenbach J., Sheng K.H., Shong C., Shong C., Sheng C., Sh
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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Gaps

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Indels

300 AA.

PRT;

PRELIMINARY;

Q9VFL4

RESULT 6 Q9VFL4 ID Q9VF1

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Q9V7U6
ID Q9V7
AC Q9V7
DT 01-M
DT 01-O
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Expressed protein, having alternative splicing products (Putative RNA pol II accessory factor) (With alternative splicing).
Name=OSJNBb0031A14.2; Synonyms=OSJNBa0034D21.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                      SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                         Annotation of the Drosophila melanogaster euchromatic genome:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003704; AAF55038.1; -.
EMBL; AY089356; AAL90094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007999; DUF745.
Pfam; PF05335; DUF745; 1.
SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;
                                                                                                                                                                                                                                                                                                                                    Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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InterPro; IPR007999; DUF745.
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                                                                                                                                                                                                                                                                                                           systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002)
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SEQUENCE FROM N.A.
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Celniker S.;
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Q75GC3
ID Q75G
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STRAIN=SCRI 1043 / ATCC BAA-672;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                           Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Fasser C.M.; Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC145387; AAR88603.1; -. EMBL; AC137991; AAS07322.1; -. SEQUENCE 375 AA; 42035 MW; 3B060F30076D2264 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Acad. Sci. U.S.A. 101:11105-11110(2004)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.9%; Score 45;
Best Local Similarity 58.8%; Pred. No. 7
Matches 10; Conservative 2; Mismatch
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InterPro; IPR010528; TolA.
Pfam; PF06519; TolA; 1.
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178 APSSARHEPSSAAAAA 194
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les 12; Conservative
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                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29471;
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01-OCT-2002
01-JUN-2003
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Q6D7F3;
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RESULT 10
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Burton G.C., Negers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Anil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Balluw R.M., Basu A., Baxendal J., Bayraktarolu L., Beasley B.M.,
Besson K.Y., Benos P.V., Barman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Buuck J., Bayraktarolu L., Beasley B.M.,
RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Evangelista C.C., Ferraz C., Ferraz C., Perriara S., Pleit Schmann W.,
RA Burtis N.L., L., Daves M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,
Alastis N.L., Harvey D., Heiman T.J., Herrandez J.R., Houston J.A.,
RA Hostin D., Houston K.A., Hawland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Katchum K.A.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
Liuk Y., Matteria N.L., Mixon K., Nixon K., Nixon D.M., Nelson D.L.,
Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri, V., Pares M. Spier E., Spradling A.C., Stapleton M., Studng R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Studng R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Studng R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Studng S., Yao Q.A., Ye H. R.,
Wang Z.Y., Wassaxman D.A., Weinstcock G.M., Weissenbach J.,
Rabber R., Robinger W., Weinscholl S., Zhan W., Saller K., Saller K., Saller W., Weinsenbach J.,
Ribbe R.A., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Zhu S.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=2245665; PubMed=12537568; Carlson J.W., Halpern A., Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
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CG6301-PA.
ORFNames=CG6301;
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Gaps
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                           Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome:
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Submitted (JUN-1997) to the PIR data bank.
PIR; S77935; S77935.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Homarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 463;
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                                                                                                                                                                                                                                                                                                                                                                  FlyBase;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0034161; CG6301.
InterPro; IPR007999; DUF745.
Pfam; PF05335; DUF745; 1.
SEQUENCE 463 AA; 49366 MW; 8D35569BEFB6EBC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 189 AA; 20180 MW; 72A4EFCD9C7ECFE9 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exoskeletal protein HACP202B (Fragment).
Homarus americanus (American lobster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exoskeletal protein HACP202A (Fragment).
Homarus americanus (American lobster).
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Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%; Score 44.5; C
61.1%; Pred. No. 44;
ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.9%; Score 45; 71.4%; Pred. No.
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| AAEKARFFQAFKAAEAAA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APEKAK-YEAYKAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003805; AAF57947.2;
IntAct; Q9V7U6; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 EKTKOAAYKAACAA 288
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 71.4
nes 10; Conservative
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Xanthomonadaceae; Xanthomonas
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                                                                                                                                                                                                                                                                                            host specificities.
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                                                                                                                                                                                                                                                                                                                                                                      Complete proteome
SEQUENCE 272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=39947;
                 NCBI_TaxID=340;
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Freyschuse B., Grandlen K.;
Freyschuse B., Grandlen K.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; X98236; CAA66888.1; -.

EMBL; X98236; CAA66888.1; -.

GO; GO:0003634; C:nucleus; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0005496; F:steroid binding; IEA.

GO; GO:00053707; F:steroid binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001292; Oestrgn_receptor.

R Pfam; PF02159; Oest_recep; 1.

R Pfam; PF02159; Oest_recep; 1.
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                1;
                                                                          Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                     Score 44.5; DB 2; Length 189;
Pred. No. 44;
4; Mismatches 2; Indels 1
          Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Homarus.
NCBI_TaxID=6706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.7%; Score 44; DB 2; Length 113; 68.8%; Pred. No. 32; ive 0; Mismatches 5; Indels
 Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca
                                                                                                                               189 AA; 20154 MW; 72A4EFCD9C647FE9 CRC64;
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113 AA; 11671 MW; A820B1196B918387 CRC64;
                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                  113 AA.
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Rattus norvegicus (Rat).
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9 AAEKARFFQAFKAAEAAA 26
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                                                                                                                                                                      54.3%;
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                                                                                                                                                       Query Match
Best Local Similarity 61.1%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 68.8
les 11; Conservative
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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Best Local S:
Matches 11
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                                                                SEQUENCE
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Q8P7P0;
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QGLAN9
ID QGLAN9
DT 05-JU
DT 05-JU
DT 05-JU
DE BELLO
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC MAMMA
OC STRAL
RA FLEYS
RL SUBMI
DR GO; G
DR FEMP;
DR FEMP;
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08P7P0
ID 08P7P
AC 08P7P
DT 01-0C
DT 01-0C
DT 01-0C
DT OT-OC
CO OC SACHE
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SEQUENCE FROM N.A.

STRAIN=ATCC 33913 / NCPPB 528;

MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Sctubal J.C., Kitajima J.P.;

"Companison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0072106.16 (Hypothetical protein P0493C06.31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.7%; Score 44; DB 2; Length 272; Best Local Similarity 66.7%; Pred. No. 75; Astches 10; Conservative 1; Mismatches 4; Indels
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Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, clone:OSJNBa0072106.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone:P0493C06.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 AA; 28377 MW; 1713145CEC084925 CRC64;
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EMBL; AP005193; BAD31146.1; -.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0030001; P:metal ion transport; IEA.
InterPro; IPR006121; HeavyMe_transpt.
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EMBL; AE012368; AAM41843.1; -.

GO; GO:0005524; F:ATP binding; IEA.

InterPro; IPR000808; Mrp.

PROSITE; PS01215; MRP; 1.
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237 APESAAAQAYLAAAA 251
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STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VDI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
EMBL; AE016930; AA076233.1; -.
InterPro; IPR005094; Relaxase.
InterPro; IPR005094; Relaxase.
Pfam; PF03432; Relaxase; 1.
Complete proteome.
SEQUENCE 316 AA; 36130 MW; B63E149ACEDEC898 CRC64;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
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                                                                             Query Match 53.7%; Score 44; DB 2; Length 306; Best Local Similarity 68.8%; Pred. No. 84; Matches 11; Conservative 1; Mismatches 4; Indels
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306 AA; 32378 MW; A60288C9B77E8868 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mobilization protein BmgA.
OrderedLocusNames=BT1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 316 AA.
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122 PEKEAAKADKAAAAA 137
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Best Local Similarity 56.2
Matches 9; Conservative
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   SEQUENCE
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ID QBA8P1
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Compugen Ltd.
version - 2005
GenCore
Copyright (c) 1993
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- protein search, using sw model OM protein March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds (without alignments) 65.338 Million cell updates/sec Run on:

1 EKPKFEAYKAAAAPA 15 US-10-056-583A-91 76 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

0B 0B

seq length: 0 seq length: 2000000000 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_16Dec04:*

geneseqp1980s:*geneseqp1990s:* geneseqp2000s:*geneseqp2001s:*

geneseqp2003as:*geneseqp2003bs:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	당선	Length	DB	ID	Descrip
-	92	100.0	15	5	ABP52297	Abp52297 HLA-DR2 m
7	73	96.1	15	Ŋ	ABP52291	Abp52291 HLA-DR2 m
e	70	92.1	15	വ	ABP52304	Abp52304 HLA-DR2 m
4	69	90.8	15	ഹ	ABP52299	Abp52299 HLA-DR2 m
ស	68	89.5	17	വ	ABP52303	Abp52303 HLA-DR2 m
9	67	88.2	15	ß	ABP52290	Abp52290 HLA-DR2 m
7	67	88.2	15	ហ	ABP52292	Abp52292 HLA-DR2 m
60	64	4	17	ហ	ABP52302	Abp52302 HLA-DR2 m
σ	63	ς.	15	ഗ	ABP52300	Abp52300 HLA-DR2 m
10	63	ς.	15	ഹ	ABP52305	Abp52305 HLA-DR2 m
11	57	ω.	15	Ŋ	ABP52271	Abp52271 HLA-DR2 m
12	57	δ.	15	ហ	ABP52289	Abp52289 HLA-DR2 m
13	57	ů.	15	Ŋ	ABP52298	Abp52298 HLA-DR2 m
14	57	S	17	ហ	ABP52294	Abp52294 HLA-DR2 m
15	57	75.0	17	ß	ABP52296	Abp52296 HLA-DR2 m
16	57	75.0	19	ស	ABP52295	Abp52295 HLA-DR2 m
17	26	73.7	15	ស	ABP52301	Abp52301 HLA-DR2 m
	53	Q,	15	Ŋ	ABP52293	Abp52293 HLA-DR2 m
	53	69.7	781	œ	ADN60395	Adn60395 B. lichen
20	23	69.7	781	80	ADN60505	Adn60505 B. lichen
	53	69.7	781	æ	ADN60519	Adn60519 B. lichen
22	51	67.1	15	Ŋ	ABP52270	Abp52270 HLA-DR2 m
	51	67.1	15	Ŋ	ABP52272	Abp52272 HLA-DR2 m
24	47	.	15	Ŋ	ABP52263	Abp52263 HLA-DR2 m
	46	60.5	299	4	ABB63276	Abb63276 Drosophil

Ad896704 Drosophil Abp52264 HLA-DR2 m Abp52267 HLA-DR2 m Abp52259 HLA-DR2 m Abb52257 HLA-DR2 m Abb23345 Protein e Abp52265 HLA-DR2 m Abp79775 N. gonorr Abu38057 Protein e Abu37170 Protein e Abb39072 Drosophil Abb52254 HLA-DR2 m Abp52255 HLA-DR2 m	
ADS96704 ABP52264 ABP52267 ABP52259 ABP52259 ABP52257 ABP73345 ABP79775 ABU38057 ADP08309 ABB59072 ABP52255 ABP52256	ABP52251 ABP52241 ABP52249 ABP52239
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ALIGNMENTS

HLA-DR2 molecule binding peptide SEQ ID NO:91. ABP52297 standard; peptide; 15 AA. anti-tumour necrosis factor agent (first entry) 16-OCT-2002 ABP52297; ABP52297

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;

sapiens Synthetic. Homo

WO200259143-A2.

01-AUG-2002.

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE.

Ξ Strominger JL, Fridkis-Hareli

WPI; 2002-608439/65.

a major treating a New compositions comprising synthetic peptides in complex with histocompatibility complex class II HLADR2 protein, useful for demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

Length 15;

Score 73; DB 5; Pred. No. 4.3e-05;

96.1%; 93.3%;

Similarity

Query Match

Sequence 15 AA;

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such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                                                                                                                   100.0%; Score 76; DB 5; Length 15; 100.0%; Pred. No. 1.4e-05; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      ABP52291 standard; peptide; 15 AA.
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                                                                                                                                     Local Similarity
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Synthetic.
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                                                                                               Sequence 15
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                                                                    invention
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                                                                                                                                                                                                                                                                                               Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent peptides used in the exemplification of the present
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                                                                                                                                                                                                                                                                     HLA-DR2 molecule binding peptide SEQ ID NO:98.
                           Mismatches
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                           1;
                                                                                                                                                                         ABP52304 standard; peptide; 15
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93.3%;
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Best Local Similarity 93.33
Matches 14; Conservative
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                                                            1 EKPKFEAYKAAAPA
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Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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1 EKPKFEAYKAAAAPA 15

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present

invention

ABP52303;

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HLA-DR2 molecule binding peptide SEQ ID NO:93.
ABP52299 standard; peptide; 15 AA.
        (first entry)
        16-OCT-2002
   ABP52299;
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent. Ξ Fridkis-Hareli 24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P (HARD) HARVARD COLLEGE Strominger JL, WO200259143-A2 sapiens. 01-AUG-2002 Synthetic. Ношо

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis. WPI; 2002-608439/65

present invention describes compositions (I) comprising a peptide Claim 28; Page 39; 54pp; English. The

with an amino acid sequence with tyrosine (Y), Iysine (K), and for valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

Sequence 15 AA;

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Gaps
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Score 69; DB 5; Length 15;
Pred. No. 0.0002;
0; Mismatches 1; Indels
90.8%;
                       14; Conservative
           Similarity
Query Match
Best Local (
                       Matches
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EKPKFEAYKAAAAPA 15 Н

EKPKVEAYKAAAPA 15

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RESULT 5 ABP52303 ID ABP5

ABP52303 standard; peptide; 17 AA.

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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                         HLA-DR2 molecule binding peptide SEQ ID NO:97.
                                                                                                       anti-tumour necrosis factor agent
                                                                                                                                                                                                                                          Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                     24-JAN-2002; 2002WO-US002071.
                                                                                                                                                                                                       24-JAN-2001; 2001US-0263569P
                          16-OCT-2002 (first entry)
                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE
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                                                                                                                         sapiens.
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                                                                                                                                  Synthetic.
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP55207 to ABP52305 represent peptides used in the exemplification of the present invention

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

WPI; 2002-608439/65.

Claim 28; Page 39; 54pp; English.

Sequence 17 AA;

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  Length 17;
                        1; Indels
Score 68; DB 5; I
Pred. No. 0.00033;
0; Mismatches 1;
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 89.5%;
93.3%;
Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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1 EKPKFEAYKAAAAPA 15 EKAKFEAYKAAAAPA 17

8 g

ABP52290 standard; peptide; 15 AA. 16-OCT-2002 (first entry) ABP52290; RESULT 6
ABP52290
ID ABP5
XX
AC ABP5
XX
DT 16-0
XX
DE HLAXX

HLA-DR2 molecule binding peptide SEQ ID NO:84.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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                                                                                                        anti-tumour necrosis factor agent
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                                                                                                                                                                                                                                                                                                                                                                                                                      Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 28; Page 39; 54pp; English
                                                                                                                                                                                                                                                                                                24-JAN-2002; 2002WO-US002071
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86.7%;
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Synthetic.
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ABP52292
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABPES207 to
                                                                                                                                                                                                                                                                                   New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
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Pred. No. 0.00042;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                   Fridkis-Hareli
                                                                                                                  24-JAN-2002; 2002WO-US002071.
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86.7%;
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                                                                                                                                                                                                                                                                                                                                      encephalomyelitis.
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                                                                                                                                                                                                                 New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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                                                                                                                            Strominger JL, Fridkis-Hareli M;
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24-JAN-2002; 2002WO-US002071
                                           24-JAN-2001; 2001US-0263569P.
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Matches 13; Conserv
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                                                                              New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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WPI; 2002-608439/65.
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us-10-056-583a-91.rag

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
                           Claim 28; Page 39; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                            invention
X8X0000000000000X8
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82.9%; Local Similarity 86.7 Les 13; Conservative Query Match Matches

1 EKPKFEAYKAAAAPA 15 1 EAPKVEAYKAAAPA 15 ð g

ABP52271 standard; peptide; 15 AA ABP52271;

(first entry) 16-OCT-2002

HLA-DR2 molecule binding peptide SEQ ID NO:65

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens. Synthetic WO200259143-A2.

01-AUG-2002.

24-JAN-2002; 2002WO-US002071

24-JAN-2001; 2001US-0263569P

(HARD) HARVARD COLLEGE

Fridkis-Hareli M; Strominger JL,

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomye $ar{1}$ itis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

ö immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present Gaps ô Length 15; 2; Indels Score 57; DB 5; Pred. No. 0.019; 1; Mismatches 75.0%; 1 EKPKFEAYKAAAPA 15 1 EKAKYEAYKAAAAA 15 Query Match Best Local Similarity 80.0° Sequence 15 AA; invention RESULT 12 ABP52289 8866666666888 ઠે q

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent. HLA-DR2 molecule binding peptide SEQ ID NO:83. (first entry) 16-OCT-2002 ABP52289;

ABP52289 standard; peptide; 15 AA.

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Gaps

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Score 63; DB 5; Length 15; Pred. No. 0.0019; 0; Mismatches 2; Indels

sapiens Synthetic Ношо

WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

(HARD) HARVARD COLLEGE

24-JAN-2001; 2001US-0263569P.

Fridkis-Hareli M;

WPI; 2002-608439/65

Strominger JL,

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis demyelinating

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

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ABP52305 represent peptides used in the exemplification of the present
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                                                                                 Length 15
                                                                                                                  2; Indels
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Pred. No. 0.019;
2; Mismatches
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                                                                                 75.0%;
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Matches 11; Conserv
                                                 Sequence 15 AA;
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Length 15;

Score 57; DB 5; Pred. No. 0.019;

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                                                                                                                                                                                                                                                                    Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                                                                                                                                                                                                                                         HLA-DR2 molecule binding peptide SEQ ID NO:88.
 Mismatches
                                                                                                                                             ABP52294 standard; peptide; 17 AA.
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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                                                                                                                                                                                                      HLA-DR2 molecule binding peptide SEQ ID NO:90.
                                                    ABP52296 standard; peptide; 17 AA.
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Synthetic.
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RESULT 15
ABP52296
ID ABP52296
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XX
DE HLA-D
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KW HLA-D
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KW HLA-D
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HOMO
OS SYNTH
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CS SYNTH
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PF 24-JA
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PP 24-JA
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Claim
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PP CHEP
CC COMPI
CC COMP
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Query Match 75.0%; Score 57; DB 5; Length 17; Best Local Similarity 80.0%; Pred. No. 0.021; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 EKPKFEAYKAAAAPA 15

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Search completed: March 31, 2005, 02:35:28 Job time : 89.7903 secs

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1 EKPKFEAYKAAAAP 14
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Sequence 16512, A
Sequence 20648, A
Sequence 17592, A
Sequence 7, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 5101, Ap
Sequence 9547, Ap
Sequence 7214, Ap
Sequence 18932, A
Sequence 14, Appl
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Sequence 1, Appl:
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                                                                     March 31, 2005, 02:26:53; Search time 22.9839 Seconds (without alignments) 48.718 Million cell updates/sec
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.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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(c) 1993 - 2005 Compugen Ltd.
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US-09-121-457-1
US-09-513-999C-5101
US-09-949-016-9547
US-09-949-016-9547
US-09-252-991A-18932
US-09-004-838-14
US-09-002-548-14
US-09-002-540-16512
US-09-248-796A-17592
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Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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76
1 EKPKPEAYKAAAAPA 15
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Perfect score:
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Maximum DB
                                                 OM protein
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APPLICANT: Buseau, Isabella
APPLICANT: Buseau, Isabella
APPLICANT: Buseau, Isabella
APPLICANT: Buseau, Isabella
APPLICANT: Wi, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITE ADDRESSE: BRANE & EMONDS
STREET: New York
COUNTRY: U.S.A.
ZIP: New York
STRATE: New York
ADDRESSE: PRADABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COUNTRY: U.S.A.
ZIP: LOGGE COMPUTER: LEM PC COMPUTER: New York
STRATIS PREDICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-21AN-1994
CLASSIFICATION NUMBER: 1306-006
TELEFAX: MISSERICE/DOCKET NUMBER: 1326-006
TELEFAX: (212) 790-9990
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         US-08-073-384C-5
US-08-254-359A-5
US-08-483-043-5
US-08-481-238-5
US-08-471-066B-5
US-08-471-066B-5
US-08-757-653-5
US-08-756-386-5
US-08-823-516-5
US-08-823-516-5
US-08-759-038-5
US-08-759-038-5
US-08-759-038-5
US-08-750-309-5
US-08-750-308-5
US-08-308-5
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                                                                                                                                                                                                                                                                                                              // Sequence 16, Application US/08185432
// Patent No. 5750652
// GENERAL INFORMATION:
// APPLICANT: Artavanis-Teakonas, Spyridon
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Gaps

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52.6%; Score 40; DB 1; Length 2471; 50.0%; Pred. No. 3.6e+02; ive 1; Mismatches 6; Indels

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RESULT 5
US-09-121-457-1
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US-08-899-232-1
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                                                                                                                                             US-08-083-590A-19

Sequence 19, Application US/08083590A

Patent No. 5786158

GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, S. et al.

TITLE OF INVENTION: Therapeutic And Diagnostic Methods

TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

TITLE OF INVENTION: Nucleic Acids

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
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Patent No. 6083904
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S. et al.
APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
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ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/083,590A

FILING DATE: 25-JUN-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REFERENCE/DOCKET NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-015

TELECOMMUNICATION INFORMATION:

TELEFAX: 212 869864/9741

TELEFAX: 212 869864/9741

TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 2471 amino acids

TVENTER ANDE: ACID ACIDS

TVENTER ANDE: ACID ACIDS

TVENTER ANDE: ACID ACIDS

TVENTER ACIDS ACIDS

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STREET: 1155 Avenue of the Americas
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50.0%;
850 ESPNFESYTCLCAP 863
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Best Local Similarity 50.07
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STRANDEDNESS: si
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STATE: New Yor)
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ZIP: 10036
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US-08-532-384-19
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| Sequence 1, Application US/08899232
| Patent No. 6436650
| GENERAL INFORMATION:
| APPLICANT: Artavanis-Tsakonas, Spyridon
| APPLICANT: Qi, Huilin
| TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
| FILE REFERENCE: 7326-046
| CURRENT APPLICATION NUMBER: US/08/899,232
| CURRENT FILING DATE: 1997-07-23
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 1
| TYPE: PRT
| TYPE: PRT
| ORGANISM: Home sapiens
| US-08-899-232-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
FILING DATE:
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 212,790-9090
TELEFAX: 212 869864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino acids
LENGTH: 2471 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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APPLICANT: Artavanis-Tsakonas, S.; APPLICANT: Qi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          850 ESPNFESYTCLCAP 863
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Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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STRANDEDNESS: si
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1 EKPKFEAYKAAAPA 15
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Best Local Similarity
7; Conserva
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-513-999C-5101
; Sequence 5101, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US 60/122,487
; PRIOR PAPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5101
· LENGTH: 75
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APPLICANT: Rand, M.
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
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                                  FILE REFERENCE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899,232
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No.
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; Patent No. 6812339
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Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-949-016-9547
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GENERAL INFORMATION:

Sequence 18932, Application US/09252991A

Sequence 18932, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7214, Application US/09489039A
Sequence 7214, Application US/09489039A
Batent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NOS: 14342
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                                                                                                                                                                                                                    Mismatches
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9547
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9547
                                                                                                                                                                            Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                          51.3%;
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illarity 58.3%;
Conservative
                                                                                                                                                                                                                                                                                         2 KPKFEAYKAAAAPA 15
                                                                                                                                                         Query Match
Best Local Similarity 64.3-
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122 PEFTAFSAAATP 133
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Best Local Similarity 46.7
Matches 7; Conservative
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181 FERFKAAAYPA 191
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Best Local Similarity
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US-09-252-991A-27869
; Sequence 27869, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                             US-09-004-838-14

Sequence 14, Application US/09004838

Patent No. 6350933

GENERAL INFORMATION:

APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.3%; Score 39; DB 3; Length 314; 63.6%; Pred. No. 55; 2; Indels 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              CTATE: Cal-
COUNTRY: USA
ZIP: 94111-3834
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1..314
; OTHER INFORMATION: /note= "RLG1D amino acids"
US-09-004-838-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
RECISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
::| : |: |||||
214 DRPAADRYRNAAAPA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 314 amino acids TYPE: amino acid
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Best Local Similarity 63.6
Matches 7; Conservative
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114 EKPKIERYEAS 124
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MOLECULE TYPE: protein
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PRIOR FILING DATE: 1999-02-18

PRIOR DATE: 1999-02-18

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PRESURT 13-11

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PRESURT 13-11

PRESURT 12-19

PRIOR DATE: 1999-02-18

PRIOR DATE: 1999-02-18

PRIOR DATE: 1999-02-18

PRESURT 10-1999-02-18

PRESURT 10-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-1999-02-19
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us-10-056-583a-91.rai

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Sequence 17592, Application US/09248796A
Sequence 17592, Application US/09248796A
Batent No. 6747137
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
APPLICATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAL
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17592
LENGTH: 260
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Pred. No. 67;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.0%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Candida albicans
US-09-248-796A-17592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 PKFEEYKA 119
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US-09-248-796A-20648

US-09-248-796A-20648

Sequence 20648, Application US/09248796A

Fatent No. 6747137

GENERAL INFORMATION:

TITLE OF INVENTION:

TORRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR PILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20648

LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknous-29-248-796A-20648
                                                                                                                                                                          Sequence 16512, Application US/09902540

Sequence 16512, Application US/09902540

Batent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Miegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: 10S/09/902,540

CURRENT FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 16512.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 4; Length 66;
Pred. No. 15;
   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
 2; Mismatches
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GORGANISM: Myxococcus xanthus
US-09-902-540-16512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Candida albicans
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Best Local Similarity 72.7
Matches 8; Conservative
7; Conservative
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515 EKPKIERYEAS 525
                                          1 EKPKFEAYKAA 11
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US-09-902-540-16512
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                                                           March 31, 2005, 02:29:23; Search time 66.5323 Seconds (without alignments)
74.648 Million cell updates/sec
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Sequence 8
Sequence 9
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                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-056-583-95
US-10-056-583-99
US-10-056-583-97
US-10-056-583-97
US-10-056-583-86
US-10-056-583-99
US-10-056-583-99
US-10-056-583-99
US-10-056-583-83
US-10-056-583-83
US-10-056-583-83
US-10-056-583-83
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                    1407402 segs, 331100923 residues
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                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                             1 EKPKFEAYKAAAAPA 15
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                                                                                                         US-10-056-583A-91
76
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Match Length
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73
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Maximum DB
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Sequence 90, Appl Sequence 89, Appl Sequence 87, Appl Sequence 64, Appl Sequence 66, Appl Sequence 51, Appl Sequence 59, Appl Sequence 59, Appl Sequence 33, Appl Sequence 34, Appl Sequence 41, Appl Sequence 62, Appl Sequence 55, Appl Sequence 52, Appl Sequence 522, Appl Sequence 523, Appl Sequence 522, Appl Sequence 523, Appl Sequence 523
US-10-056-583-90 US-10-056-583-99 US-10-056-583-89 US-10-056-583-87 US-10-056-583-64 US-10-056-583-66 US-10-056-583-57 US-10-056-583-57 US-10-056-583-51 US-10-056-583-51 US-10-056-583-51 US-10-056-583-59 US-10-056-583-59 US-10-056-583-33 US-10-056-583-34 US-10-056-583-34 US-10-056-583-34 US-10-056-583-34 US-10-056-583-34 US-10-056-583-34 US-10-056-583-48 US-10-056-583-49 US-10-056-583-49 US-10-056-583-62 US-10-056-583-62 US-10-056-583-63
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ALIGNMENTS

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Gaps
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US-10-056-583-91

US-10-056-583-91

Sequence 91, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 15

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 76; DB 14; Length 15; 100.0%; Pred. No. 2.5e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EKPKFEAYKAAAPA 15
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Best Local Similarity 100.0
Matches 15; Conservative
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RESULT 2 US-10-056-583-85

Appl Appl Appl

Sequence Sequence

Sequence Sequence Sequence

us-10-056-583a-91.rapb

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US-10-056-583-84
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0
Sequence 85, Application US/10056583

Publication No. US2003064915A1

GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 85

LENGTH: 15

LENGTH: 15

LENGTH: 15
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Sequence 98, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: TOODITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

NUMBER OF SEQ ID NOS: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.1%; Score 73; DB 14; Length 15; ilarity 93.3%; Pred. No. 8.2e-06; Conservative 1; Mismatches 0; Indels
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US-10-056-583-93
; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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nes 14; Conservative
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nes 14; Conserv
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LENGTH: 15
TYPE: PRT
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Best Local S:
Matches 14
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US-10-056-583-97

Sequence 97, Application US/10056583

Publication No. US20030064915A1

GENERAL INPORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 17
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT APPLICATION NUMBER: 00/2-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence; FEATURE: ; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
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Sequence 84, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.8%; Score 69; DB 14;
Best Local Similarity 93.3%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 89.5%; Score 68; DB 14;
Best Local Similarity 93.3%; Pred. No. 6.9e-05;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Query Match
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APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT APPLICATION NUMBER: 0/24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 96, Application US/10056583;
Publication No. US20030064915A1;
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
ITILE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
ITILE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
                                                                                                                                                                                                                          ; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-86
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Pred. No. 9e-05;
                                                                                                                                                                                                                                                                                            88.2%; Score 67; DB 14; Length 15; 86.7%; Pred. No. 9e-05;
                                                                                                                                                                                                                                                                                                                                           1; Indels
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Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84
LENGTH: 15
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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EAPKYEAYKAAAAPA 15
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Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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; Sequence 99, Application Wo. US20030064915A1
; Fublication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Presidents and Fellows of Harvard College;
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
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; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-94
                                                                                                                                                                                                       Length 17;
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86.7%; Pred. No. 0.00044;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                       Score 64; DB 14;
Pred. No. 0.00034;
                                                                                                                                                                                                                                                        1; Mismatches
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; Sequence 94, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
SEQ ID NO 96
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                     Query Match 84.2%;
Best Local Similarity 86.7%;
Matches 13; Conservative
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1 EKPKEEAFKAAAAPA 15
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Matches 13; Conservative
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Sequence 90, Application US/10056583

Sequence 90, Application US/20030064915A1

Bublication No. US20030064915A1

GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-01.
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 90

LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.0%; Score 57; DB 14; Length 17; Best Local Similarity 80.0%; Pred. No. 0.0056; Matches 12; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-90
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
               Indels
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                                                                                                                                                                                                                            Sequence 88, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
                   5
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Pred. No. 0.0056;
                 Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 88
LENGTH: 17
                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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                                                              1 EKPKFEAYKAAAPA 15
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1 EAPAYKAYKAAAAPA 15
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                 11; Conservative
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US-10-056-583-88
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US-10-056-583-90
                 Matches
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US-10-056-583-83
; Sequence 83, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Bresidents and Fellows of Harvard College
; APPLICANT: Eridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRI
CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Predents and Fellows of Harvard College,
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
TITLE OF INVENTION: CONDITIONS
TITLE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-83
                                                                                 Score 63; DB 14; Length 15;
Pred. No. 0.00044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.0%; Score 57; DB 14; Length 15; Best Local Similarity 80.0%; Pred. No. 0.0048; Matches 12; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; DB 14; Length 15; Pred. No. 0.0048;
                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                  US-10-056-583-65; Sequence 65, Application US/10056583; Publication No. US20030064915A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 65
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                               Query Match 82.9%;
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |:|||||||| |
1 EKAKYEAYKAAAAA 15
                                                                                                                                                                                EKPKFEAYKAAAPA 15
                                                                                                                                                                                                                          1 EAPKVEAYKAAAPA 15
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Best Local Similarity
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RESULT 15
US-10-056-583-89
is Sequence 89, Application US/10056583
js Publication No. US20030064915A1
js Publication No. US20030064915A1
js GENERAL INFORMATION:
js APPLICANT: Strominger, Jack L.
js APPLICANT: Fridkis-Hareli, Masha
jt TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
jt TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
jt TITLE OF INVENTION: CONDITIONS
jt TITLE OF INVENTION: CONDITIONS
jt CURRENT APPLICATION NUMBER: US/10/056,583
jt CURRENT FILING DATE: 2002-01-24
jt PRIOR FILING DATE: 2001-01-24
jt PRIOR FILING DATE: 2001-01-24
jt NUMBER OF SEQ ID NOS: 99
jt SOFTWARE: FastSEQ for Windows Version 4.0
jt SEQ ID NO 89
jt LENGTH: 19
jt TYPE: PRT
jt ORGANISM: Artificial Sequence
jt FRATURE:
jt ORGANISM: Artificial Sequence
jt FRATURE:
jt OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.0%; Score 57; DB 14; Length 19; Best Local Similarity 80.0%; Pred. No. 0.0063; Matches 12; Conservative 1; Mismatches 2; Indels
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Search completed: March 31, 2005, 02:48:48 Job time : 66.5323 secs

1 EKPKFEAYKAAAAPA 15

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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

March 31, 2005, 02:26:17; Search time 17.9032 Seconds (without alignments) 80.614 Million cell updates/sec

US-10-056-583A-91 76

EKPKFEAYKAAAAPA 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 08 08 08 Minimum Maximum

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		dp			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
: - ਜ -	44		193	-	MOMS4E	myosin alkali liqh
7	43	56.6	306	N	G96014	hypothetical profe
n	43		336	7	B81081	•
4	43		336	~	E81863	tryptophan-tRNA li
Ŋ	43		389	~	G87332	hypothetical prote
9	42.5		316	N	T14643	1-aminocyclopropan
7	42	55.3	270	~	T31225	traf protein homol
80	42		554	~	S68365	(+)-delta-cadinene
6	42		554	~	868366	(+)-delta-cadinene
10	41		185	Н	MOCH4E	
11	41		193	Н	MORT4E	myosin alkali ligh
12	41		194	7	T14644	ы
13	41	53.9	200	~	T48130	hypothetical prote
14	41		216	~	AG3508	щ
15	41		398	~	T21061	hypothetical prote
16			321	~	T07922	1-an
17	40		461	~	AI3358	pyruvate dehydroge
18	40		765	~	T15447	hypothetical prote
19			891	~	AC3384	
20	39		73	~	S40015	phd protein - phag
21			114	~	G81353	hypothetical prote
22			168	~	A45943	vitelline membrane
23			197		MOHU4 B	myosin alkali ligh
24			215	~	AG3392	maleylpyruvate iso
25		•	239	~	C44954	fumarate reductase
56		51.3	310	~	T09733	1-aminocyclopropan
27		•	321	~	T02754	probable 1-aminocy
28		•	334	-	DEQYG	glyceraldehyde-3-p
29		•	334	N	E75153	glyceraldehyde 3-p

probable glycerald phosphate-binding	C-22 sterol destu hypothetical prote probable cell surf	probable oxidoredu hypothetical prote hypothetical prote	50S ribosomal prot 50S ribosomal prot homeotic protein H	ABC transporter AT homeotic protein H 1-aminocyclopropan	hypothetical prote
G71194 C70473 D83598	S54015 T29657 AE1479	C95401 T00039 G97151	F97683 AF2908 IS0145	E86691 A43562 T10817	B86255
212	000	000	000	0 0 0	~
334 337 465	538 538 656	810 906 50	179 179 188	269 289 308	320
51.3 51.3	51.3 51.3 51.3	51.3 50.7 50.0	50.0 50.0	50.0 50.0	50.0
5 6 6 6 6 6	1 0 0 0 1 0 0 0	38.5 38	8 8 8 8 8 8	8 8 8 8 8 8	38
30	1 E E E 1 E E E 1 E E E	36 38 38	39 4 4 1 0	4 4 4 2 6 4	45

ALIGNMENTS

RESULT I

MOMS4E
myosin alkali light chain 4, embryonic and atrial - mouse
N;Alternate names: MLC1A; MLC1emb; myosin L1 catalytic light chain, atrial
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence revision 03-Oct-1995 #text change 09-Jul-2004
C; Accession: A31114; S01944
R; Barton, P.J.R.; Robert, B.; Cohen, A.; Garner, I.; Sassoon, D.; Weydert, A.; Buckingha
J. Biol. Chem. 263, 12669-12676, 1988
A, Title: Structure and sequence of the myosin alkali light chain gene expressed in adult
A; Reference number: A31114; MUID:88315068; PMID:2842339
 A; Accession: A31114

A;Residues: 1-193 <BAR>
A;Cross-references: UNIPROT: P09541; GB:M20772; GB:J03932; GB:M19435; NID:g199731; PIDN:A
R;Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.
Nucleic Acids Res. 16, 10037-10052, 1988
A;Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striate
A;Reference number: S01944; MUID:89057447; PMID:3194193

A;Accession: S01944 A;Molecule type: DNA A;Residues: 1-41 <COH>

A; Conserved to the form is found in fetal and regenerating skeletal muscle, fet C; Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet C; Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet C; Genetics:
A; Introns: 41/3; 51/1; 101/1; 159/1; 185/1
C; Superfamily: calmodulin; calmodulin repeat homology
C; Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contrac F; 47-81/Domain: calmodulin repeat homology < EF1>
F; 126-158/Domain: calmodulin repeat homology < EF4>

Gaps ö 57.9%; Score 44; DB 1; Length 193; 71.4%; Pred. No. 4; tive 1; Mismatches 3; Indels Query Match Best Local Similarity 71.4: Watches 10; Conservative

.. 0

2 KPKFEAYKAAAAPA 15 g ઠ

RESULT 2 G96014

hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB C; Species: Sinorhizobium meliloti C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: G96014
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G96014

```
C; Accession: G87332
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.E; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolone B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nighternate names: ACC oxidase
(Species: Sorghum bicolor (sorghum)
(Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
(Spacession: T14643
(Spacession: T1643)
(Spacession: T16443)
(Spacession: T16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-316 <FIN>
A;Cross-references: UNIPROT:081606; EMBL:AF079588; NID:g3386564; PIDN:AAC28488.1; PID:g3:C;Genetics:
A;Gene: ACO1
C;Function:
                                                          GB:AL157959; NID:g7380091; PIDN:CAB84910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9AAC8; GB:AE005673; NID:g13421893; PIDN:AAK22659.1; GSPDB:GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: catalyzes the reaction of 1-aminocyclopropane-1-carboxylic acid, oxygen ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-) ACO1 [similarity] - sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein CC0674 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                         Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 2; Length 389;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Pathway: ethylene biosynthesis
C.Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C.Keywords: ethylene biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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                                                                                                                                                                                                                                                                                                                                         2;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
                                             A;Cross-references: UNIPROT:Q9JTQ0; GB:AL162756;
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: trpS; NMA1682
C;Superfamily: tryptophan-tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                      DB
10;
                                                                                                                                                                                                                                                                                                                                      56.6%; Score 43; DB 53.3%; Pred. No. 10; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 ESPLFEIYKAFSTPS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EKPKFEAYKAAAAPA 15
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Best Local Similarity 53.3<sup>3</sup>
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                      A; Residues; 1-336 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-389 <STO>
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A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: CC0674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues:
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-306 < KUR>
A; Residues: 1-306 < KUR>
A; Residues: 1-306 < KUR>
A; Cross-references: UNIPROT: Q92TW2; GB: AL591985; PIDN: CAC49783.1; PID: g15141270; GSPDB: GA; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Contents: annotation
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tryptophanyl-tRNA synthetase NMB1471 [imported] - Neisseria meningitidis (strain MC58 se C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: B81081 C;Accession: B81081 C;Accession: B81081 C;Accession: B81081 C;Accession: B81081 C;Fieischmann, R.D.; Dougherty, B.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; H.; A.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
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A;Experimental source: serogroup B, strain MC58
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R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Titler: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A; Reference number: A81775; MUID:20222556; PMID:10761919
A; Ratus: preliminary
A; Molecule type: DNA
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5; Mismatches
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Pred. No.
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C,Superfamily: tryptophan-tRNA ligase
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57.1%;
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RPQPEAFESAAAPA 79
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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55.3%; initarity 61.5%; Conservative 1,
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9; Conserva
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les 8; Conserv
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C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T31225
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati A;Reference number: Z20992
A;Accession: T31225
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T31225
A;Kesidues: 1-270 <ROM>
A;Residues: 1-270 <ROM>
A;Residues: 1-270 <ROM>
A;Residues: 1-270 <ROM>
A;Cross-references: UNIPROT:085933; EMBL:AF079317; NID:g3378261; PID:g3378366; PIDN:AADGC;Genetics:
A;Genome: plasmid pNL1
A;Note: traf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.) delta-cadinene synthase isozyme XC1 - Gossypium arboreum
C; Species: Gossypium arboreum
C; Species: Gossypium arboreum
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C; Accession: S68365
R; Chen, X.Y.; Chen, Y.; Heinstein, P.; Davisson, V.J.
Arch. Blochem. Biophys. 324, 255-266, 1995
A; Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat
A; Reference number: S68365; MUD: 96132653; PMID: 8554317
A; Accession: S68365, MUD: 96132653; PMID: 8554317
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-554 < CHE>
A; Cross-references: UNIPROT: Q39761; EMBL: U23206; NID: g1045311; PIDN: AAA933064.1; PID: g104
A; Experimental source: cultivar Nanking
C; Superfamily: vetispiradiene synthase 1
C; Keywords: phytoalexin biosynthesis
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C;Species: Gossypium arboreum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68366
R;Chen, X.Y.; Chen, Y.; Heinstein, P.; Davisson, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A;Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase:
A;Reference number: S68365; MUID:96132653; PMID:8554317
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 Indels
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Pred. No. 12;
0; Mismatches
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1; Mismatches
Mismatches
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298 KEPRFEAVKAAAPKSSPA 315
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
Conservative
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A;Molecule type: mRNA
A;Residues: 1-554 <CHE>
A;Cross-references: UNIPROT:Q39760; EMBL:U23205; NID:g1045313; PIDN:AAA93065.1; PID:g104
A;Experimental source: cultivar Nanking
C;Superfamily: vetispiradiene synthase 1
C;Keywords: phytoalexin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin alkali light chain 4, embryonic - chicken
N;Alternate names: myosin L23 catalytic light chain
C;Species: Gallus (chicken)
C;Species: O1-Dec-1989 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Date: 01-Dec-1989 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: S02065; A29473
R;Nabeshima, Y.I.; Nabeshima, Y.; Kawashima, M.; Nakamura, S.; Nonomura, Y.; Fujii-Kuriy J. Mol. Biol. 204, 497-505, 1988
A;Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic gi A;Reference number: S02065; MUID:89141751; PMID:3225843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 262, 14408-14414, 1987
A;Title: A common myosin light chain is expressed in chicken embryonic skeletal, cardiac
A;Reference number: A29473; MUID:88032983; PMID:3667580
A;Accession: A29473
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A, Residues: 1-93,'L',95-165,'L',167-185 <KAW>
A, Cross-references: GB:J02823; NID:g212339; PIDN:AAA48957.1; PID:g212340
A, Note: the authors translated the codon CTG for residue 94 as Met and TAC for residue 1
C, Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac
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Nucleic Acids Res. 18, 1581-1586, 1990
A;Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of expressi
A;Reference number: S09236; MUID:90221887; PMID:2326197
A;Accession: S09236
A;Molecule type: mRNA
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C;Complex: The myosin molecule contains two heavy chains, two alkali light chains, and t
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: brain; calcium binding; duplication; EF hand; muscle contraction
F;39-73/Domain: calmodulin repeat homology <EF1>
F;118-150/Domain: calmodulin repeat homology <EF3>
F;153-185/Domain: calmodulin repeat homology <EF4>
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N;Alternate names: MLC1A; MLC1emb; myosin L1 catalytic light chain, atrial
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: S09236
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A, Residues: 1-185 < NAB>
A, Cross-references: UNIPROT: P09540; EMBL: X14428
A, Note: the authors translated the codon CGG for residue 71 as R; Kawashima, M.; Nabeshima, Y.; Obinata, T.; Fujii-Kuriyama, Y.
                                                                                                                                                                                                                                                                                     Length 554;
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                                                                                                                                                                                                                                                                               Score 42; DB 2
Pred. No. 25;
1; Mismatches
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C; Genetics:
           Matches
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A; Residues: 1-193 <ROV>
A; Cross-references: UNIPROT: P17209; EMBL: X51531; NID: 957512; PIDN: CAA35911.1; PID: 957513
C; Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet C; Superfamily: calmodulin; calmodulin repeat homology
C; Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract F; 47-81/Domain: calmodulin repeat homology <EF1>
F; 126-158/Domain: calmodulin repeat homology <EF3>
F; 161-193/Domain: calmodulin repeat homology <EF4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-) ACO2 - sorghum (fragment)
N;Alternate names: ACC oxidase
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14644
R;Finlayson, S.A.; Lee, I.J.; Mullet, J.E.; Morgan, P.W.
Plant Physiol. 119, 1083-1089, 1999
A;Title: The mechanism of rhythmic ethylene production in sorghum. The role of phytochrc A;Reference number: Z18166; MUID:99169299; PMID:10069847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
T48130
hypothetical protein T4C9.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48130
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew submitted to the Protein Sequence Database, June 1999
A;Reference number: Z24485
A;Accession: T48130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:O81607; EMBL:AF079589; NID:g3386566; PIDN:AAC28489.1; PID:g3
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                                                                                                                                                                                                                                                         Query Match 53.9%; Score 41; DB 1; Length 193; Best Local Similarity 64.3%; Pred. No. 13; Matches 9; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: involved in ethylen biosynthesis
A;Pathway: ethylene biosynthesis
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C;Keywords: ethylene biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9STJ1; EMBL:AL080318
A;Experimental source: cultivar Columbia; BAC clone T4C9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-194 <FIN>
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Pred. No. 13;
4; Mismatches
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Best Local Similarity 53.3%;
Matches 8; Conservative
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KEPRFEAMKSAIATA 194
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-200 <BEV>
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitenss: A;Reference number: AD3252; PMID:11756688
A;Accession: AG3508
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-216 <KUR>
A; Cross-references: UNIPROT: Q8YE25; GB: AE008917; PIDN: AAL53234.1; PID: g17984111; GSPDB:GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P54412; EMBL:Z72507; PIDN:CAA96631.1; GSPDB:GN00023; CESP:F15.
A;Experimental source: clone F17C11
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21061
R;McMurray, A.
Submitted to the EMBL Data Library, May 1996
A;Recession: T21061
A;Accession: T21061
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-398 *MLL>
                                                                                                                                                                                                                                                                     C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AG3508
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                                                                                                                                                                                                                                           transporter BMEI2053 [imported] - Brucella melitensis (strain 16M)
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Pred. No. 15;
2; Mismatches 3; Indels
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Pred. No. 27;
0; Mismatches 3; Indels
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C;Superfamily: translation elongation factor eEF-1 gamma chain
  Indels
    4
Mismatches
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Job time : 18.9032 secs
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ilarity 76.9%;
Conservative
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Best Local Similarity 52.6%;
Matches 10; Conservative
                                                                                                       180 EKPKEHAYKAQEA 192
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                                                  1 EKPKFEAYKAAAA 13
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9; Conservative
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Best Local Similarity
Matches 10; Conserv
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A;Gene: CESP:F17C11.9
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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

March 31, 2005, 02:18:02; Search time 80.5645 Seconds (without alignments) 95.342 Million cell updates/sec Run on:

US-10-056-583A-91 76 Title: Perfect score:

1 EKPKFEAYKAAAAPA 15 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q65jq3 bacillus li	P50887 drosophila	Q9uan1 drosophila		w	homo	homo	น ธกพ	Ġ	Q7vzx6 bordetella	Q7w1p2 bordetella	Q7wq18 bordetella	Q92tw2 rhizobium m	Q9jtq0 neisseria m	Q9jyq9 neisseria m	Q9aac8 caulobacter	Q7nvt5 chromobacte	Q8sxm8 drosophila	Q9w327 drosophila	Q89p82 bradyrhizob		Q6jrs4 equus cabal		O85933 sphingomona		Q63v82 burkholderi	Q88nk4 pseudomonas				
ID	Q65JG3	RL22 DROME	Q9UAN1	Q7SDS7	Q7UTK6	069YQ8	60X690	MLEF MOUSE	P933 <u>2</u> 6	9XZALQ	Q7W1P2	Q7WQL8	Q92TW2	SYW NEIMA	SYW_NEIMB	Q9AAC8	Q7NVTS	Q8SXM8	Q9W327	Q89P82	081606	Q6JRS4	SSB SHEON	085 <u>9</u> 33	Q62L76	Q63V82	DPO4_PSEPK	Q9SW77	09LKN1	DCS1 GOSAR	דעפטק "נפטע
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% Query Match	69.7	60.5	60.5	60.5	59.5	59.2	59.5		57.9	57.9	57.9	57.9	56.6	56.6	56.6	ė.	56.6	26.6	9.95	9.95	55.9	55.3	55.3		55.3	55.3	55.3	55.3	55.3	55.3	ני
Score	53	46	46	46	45	45	45	44	44	44	44	44	43	43	43	43	43	43	43	43	42.5	42	42	42	42	42	42	42	42	42	4.2
Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17		19	20			23		25	56	27	28	29	30	7.

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PS08B7; Q9V3X9; O1-OCT-1996 (Rel. 34, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update) 60S ribosomal protein L22.

299 AA.

PRT;

STANDARD;

DROME

Q39760 gossypium a O49853 gossypium a	Q6bug2 debaryomyce Q8fri5 corynebacte	Q8kg95 chlorobium P09540 qallus qall	P17209 rattus norv	O81607 sorghum bic	Q9stjl arabidopsis		Q8fy17 brucella su			
DCS2_GOSAR DCS4_GOSAR	Q6BU <u>Q</u> 2 Q8FR15	Q8KG95 MLEX CHICK	MLEF_RAT	081607	Q9STJ1	Q8YE25	Q8FY17	Q892F2	Q6JN53	Q814K9
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554 554	1304	143 185	192	194	200	216	235	249	317	373
55.3	55.3 53.9	53.9	53.9	53.9	53.9	53.9	53.9	53.9	53.9	53.9
4 4 2 4	4 4 1 1 2	4 1 1 1	41	41	41	41	41	41	41	41
32 33	34 35	36 37	38	39	40	41	42	43	44	45

ALIGNMENTS

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L U. ......

L U. ......

L U. ......

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L SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky B.J.,

RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,

RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,

RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,

RA Berka R.M.;

RY "Complete genome sequence of the industrial bacterium Bacillus

RT "Complete genome comparisons with closely related Bacillus species.";

RT Iicheniformis and comparisons with closely related Bacillus species.";

RL Genome Biol. 5:R77-R77(2004).

DR EMBL; AB017333; AAU40801.1; -.

DR EMBL; CP000002; AAU23441.1; -.

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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=DSM 13;
PubMed=15383718;
Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
Ehrenreich A., Gottschalk G.;
"The Complete Genome Sequence of Bacillus licheniformis DSM13, organism with Great Industrial Potential.";
"Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
SpoIIE (DNA translocase).
Name=spoIIIE; ORFNames=BL01204, BLi01906;
Bacillus licheniformis DSM 13.
Bacillus licheniformis Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=279010;
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66.7%; Pred. No. 2.6;
iive 3; Mismatches
  781 AA
  PRT;
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264 EKPEVQAYEAPAAPA 278
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Matches 10; Conservative
PRELIMINARY;
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AC P508@7;
DT 01-OCT-
DT 25-JAN-
DE 60S rib
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REPEQUANCE FROWN N.A.

RECURSER F.A. Lewis S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA BERODGO R.C., ROGER Y.-H.C., Blazej F.G., Champe M., Feliffer B.D.,

RA ADII J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

Ballew R.M., Dayle C., Barrer E.G., Helt G., Nelson C.R., Miklos G.I.G.,

RA BADIL J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

Ballew R.M., Camper B.D., Burchan M.R., Bouck J., Byraktaroglu L., Bosaley E.M.,

Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Botelier P.,

RA Berkoya D., Botchan M.R., Bouck J., Byroktein P., Brottler P., Brottler P.,

RA Berkoya D., Gorden M.R., Bouck J., Byroktein P., Brottler P., Brottler P.,

RA Grary J.M., Camper S., Dang Z., Mays A.D., Dew I., Dietz S.M.,

RA Grary J.M., Camper S., Dang Z., Mays A.D., Dew I., Dietz S.M.,

RA Grary J.M., Camper S., Dennes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Bouchin K.J., Barvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marvey D.A., Holland T.J., Mein. H., Ibegwam C.,

Liu X., Mattel B. McIncoh T.C., McLeod M.D., McBron D.L.,

RA Harris N.L., Mattel B. McIncoh T.C., McLeod M.D., McHerson D.,

RA Milliama N.W., McDatry C., Morisol J., Mang D., Santh T.,

Spier E., Spradding A.C., Stanpson M., Stupski M.P., Santh T.,

Spier E., Spradding A.C., Stanpson M., Stupski M.P., Santh T.,

Spier E., Spradding A.C., Stanpson M., Stupski M.P., Santh T.,

RA Palazzolo M., Pittman G.S., Pan, McM. Shore E., Shen H.,

Raber S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O., Zheng L.,

RA Benner K., Menington K.A., Rubarker B.,

Raber S.M., Woodage T., Worley K.C., Wu D., Yang
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MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
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MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Annotation of the Drosophila melanogaster euchromatic genome: a
                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                         Glover C.V.C., Bidwai A.P., Zhao W.F.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 Name=RpL22; ORFNames=CG7434;
                                                                                                                                                                  SEQUENCE FROM N.A. .
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                                                                                                                NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0; Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.; "Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal proteins, L22 and 123a, with unique histone-like amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C., Glover D.M.;
                                                                                                  "From sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                         melanogaster.";
Science 287:2220-2222(2000).
-!- SIMILARITY: Belongs to the ribosomal protein L22e family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oguani;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein L22 (Fragment).
Name=RpL22; Synonyms=rpl22;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asp/Glu-rich (highly acidic). 46A99005610E4EB0 CRC64;
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Pred. No. 17;
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73.3%; Pred. No. 1.,
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Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
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EMBL; AF080131; AAD19341.1; -.

FlyBase; FBgn0015288; RpL22.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005840; C:ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002671; Ribosomal L22e.
Pfam; PF01776; Ribosomal L22e; 1.
ProDom; PD007306; Ribosomal L22e; 1.
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EMBL; AE003418; AAF45546.1; -.
EMBL; AL132792; CAB60023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30610 MW;
                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0015288; RpL22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EKPKFEAYKAAAAPA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.5
Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                     IntAct; P50887; -
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Rhodopirellula baltica.
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Q69YQ9;
25-OCT-2004
25-OCT-2004
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Q69YQ8
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ID Q6
AC Q6
DT 25
DT 25
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OS HC
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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

A Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

Balkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

Balkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

A Qui D., Ianakiev P., Redersen D., Nelson M., Washburne M.,

A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

Rothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

A Kamal M., Ramwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;

"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 0:0-0(2003).

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABX01000044; EAA34940.1; -.
SEQUENCE 458 AA; 49949 MW; 196D609BF9320496 CRC64;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR002671; Ribosomal_L22e.
Fram; PF01776; Ribosomal_L22e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%; Score 46; DB 2; Length 458; 66.7%; Pred. No. 25; 3; Indels iive 2; Mismatches 3; Indels
                                                                                                                                                           4; Indels
                                                                                        312 AA; 32273 MW; 0BE9A15CB473083B CRC64;
                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                          60.5%; Score 46; DB 73.3%; Pred. No. 17; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Created)
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01-MAR-2004 (TrEMBLrel. 26, L
01-MAR-2004 (TrEMBLrel. 26, L
Predicted protein.
                                                                                                                                                                                       1 EKPKFEAYKAAAAPA 15
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                                                                                                                                                                                                                      49 ЕКРКАЕААКРАААА 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 OKPKOKAAKAKAPA 92
                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
OrderedLocusNames=RB3828;
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                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                          Query Match
Best Local Similarity
Matches 11; Conserva
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Matches 10; Conserv
                                                              Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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Q7UTK6
ID Q7UTY
AC Q7UTY
DT 01-0C
DT 01-CC
DT 01-CC
DT 01-CC
DT O1-CC
DT O1-CC
DT O1-CC
DT O1-CC
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Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                      MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Skeletal muscle;
TISSUE=Skeletal muscle;
TISSUE=Skeletal muscle;
The German cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AL832376; CAH10402.1; -.
Hypothetical protein.
NON TER 1340 1340
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 2; Length 800; Pred. No. 63; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

EMBL; BX294139; CAD73430.1; -.

InterPro; IPR001345; PG/BPGM mutase.

PROSITE; PS00175; PG MUTASE; UNKNOWN 1.

Complete proteome; Hypothetical protein.

SEQUENCE 800 AA; 91385 MW; C32C861687CDB466 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp4511127 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp451A076 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.2%; Score 45; DB 2; 64.3%; Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.2%; Score 45; 57.1%; Pred. No.
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773 KPAWDAYKSIATPA 786
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Best Local Similarity 64.3.,
-hes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88315068; PubMed=2842339;
Barton P.J.R., Robert B., Cohen A., Garner I., Sassoon D., Weydert A.,
Buckingham M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skeletal and ventricular muscle.
-1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS PROTEIN DOES NOT BIND CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Promoter analysis of myosin alkali light chain genes expressed in mouse striated muscle.";
Nucleic Acids Res. 16:10037-10052(1988).
-!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                   SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
TISSUE=Skeletal muscle;
The German cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AL832347; CAH10406.1; -.
Hypothetical protein.
NON_TER 1614 1614
                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: Expressed in atrial muscle and in fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure and sequence of the myosin alkali light chain gene expressed in adult cardiac atria and fetal striated muscle."; J. Biol. Chem. 263:12669-12676(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Myosin light chain 1, atrial/fetal isoform (MLCIA) (MLCIEMB).
Name=Mlcla; Synonyms=Myla;
                                                                                                                                                                                                                                                                        Score 45; DB 2; Length 1614; Pred. No. 1.2e+02; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89057447; PubMed=3194193;
Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
Buckingham M.E.;
                                                                                                                                                                                                                                      1614 AA; 175041 MW; FCE219C927BAEB9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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EMBL; M31017; AAA39721.1; JOINED.
EMBL; M20769; AAA39721.1; JOINED.
                                                                                                                                                                                                                                                                        59.2%;
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562 ENEEFEAYSPAAAP 575
                                                                                                                                                                                                                                                                                                                                                1 EKPKFEAYKAAAAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-40 FROM N.A.
                                                                                                                                                                                                                                                                                        Local Similarity 64.3 hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                NCBI_TaxID=9606;
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MLEF_MOUSE
ID MLEF_MOUSE
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                                                                                                                                                                                                                                  SEQUENCE
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-!- SIMILARITY: Belongs to the iron/ascorbate-dependent oxidoreductase
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Musa acuminata (Banana).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
Spermatophyta, Magnoliophyta, Liliopsida, Zingiberales, Musaceae,
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Alcaligenaceae; Bordetella.
                                                                                                                                                                                                        Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%; Score 44; DB 2; Length 315; ilarity 57.1%; Pred. No. 38; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                            192 AA; 21028 MW; B0439D512FA19C38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X95599; CAA64856.1; -.
HSSP; Q96323; 1GP6.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005123; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy; Î.
Iron; Oxidoreductase.
SEQUENCE 315 AA; 35348 MW; 9EA22912E6F0BE43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 1-aminocyclopropane-1-carboxylate oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable GTP-binding protein.
OrderedLocusNames=BP0747;
Bordetella pertussis.
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                                                                                                                                                                                                       Score 44; DB 3 Pred. No. 24; 1; Mismatches
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                                                                                   MGD; MGI:97267; Myla.
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF Hand like.
ProDom; PD000012; EF-hand; 2.
Multigene family; Muscle protein; Myosin.
INIT MET
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3L; M20770; AAA39721.1; JOINED.
3L; M20771; AAA39721.1; JOINED.
3L; X12971; CAA31414.1; -.
3L; M19436; AAA39720.1; -.
3; A31114; MOMS4E.
3; P02607; 1BR1.
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                                                                                                                                                                                                      Query Match 57.9%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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298 KEPRFEAMKATALP 311
                                                                                                                                                                                                                                                                2 KPKFEAYKAAAAPA 15
                                                                                                                                                                                                                                                                                            6 ЕРККЕААКРААРА 19
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Les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4641;
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=bacol
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EMBL;
EMBL;
EMBL;
EMBL;
                                                       PIR; A
HSSP;
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Q7VZX6
ID Q7VZX
AC Q7VZX
DT 01-0C
DT 01-MA
DE Proba
GN Order
OS Borde
OC Bacte
OC Alcal
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Query Match
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AC Q7WQL8

DT O1-OCT-2

DT O1-OCT-2

DT O1-DCT-2

DE Probable

GN Orderedid

OX NCBI Tan

RN Bordetel

RA Parkhill

RA Parkhill
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Q92TW2
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=12822 / ATCC BAA-587;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Rathill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

A Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Atkin R., Temple L., James K.D., Harris B., Quail M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Rebtinowits P., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"The following the follows of the genome sequences of Bordetella pertussis,

"The follows the follows the
                                                                                                                                          MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Marris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Beather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
A Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
A Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
The Comparative analysis of the genome sequences of Bordetella pertussis,
The Comparative analysis of the genome sequences of Bordetella pertussis,
The Control of the Genome sequences of Bordetella pertussis,
The Control of the Genome sequences of Sordetella pertussis,
The Control of the Genome sequences of Sordetella pertussis,
The Control of the Genome sequences of Sordetella pertussis,
The Control of the Genome sequences of Sordetella pertussis,
The Control of the Genome sequences of Sordetella pertussis,
The Control of the Genome sequences of Sordetella pertussis,
The Comparative of the Genome sequences of Sordetella pertussis,
The Comparative of the Genome sequences of Sordetella pertussis,
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Alcaligenaceae, Bordetella.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable GTP-binding protein.
OrderedLocusNames=BPP0309;
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EMBL; BX640413; CAE41053.1; -.

HSSP; P44681; 1JAL.

GO; GO:0005525; F:GTP binding; IEA.

InterPro; IPR006074; GTP1/OBG_dom.

InterPro; IPR006169; GTP1_OBG_Bub.
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InterPro; IPR006074; GTP1/OBG dom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR002917; MAR HSRI.
Pfam; PF01018; GTP1 OBG; 1.
Pfam; PF01926; MMR HSRI; 1.
PROSITE; PS00905; GTP1_OBG; 1.
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EMBL; BX640423; CAE40050.1; -.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Q7W1P2
ID Q7W1P2
DT 01-OC
DT 01-OC
DT 01-MA
DE Proba
GN Order
OC Alcal
OX NCBI
RN [1]
RN FSQUE
RC STRAII
RX MEDLI
RA Harri
RA Achtm
RA Achtm
RA Cerde
RA Achtm
RA Cerde
RA Cerde
RA Achtm
RA Cerde
RA CERDIII
RA CERDII
OX
REAL REAL BRIT BRIT BRAND DR REAL BRAND D
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=RB50 / ATCC BAA-588;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"Comparative analysis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                Gaps
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OrderedLocusNames=BB0312;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                    Length 377;
InterPro; IPR006169; GTP1_OBG_Bub.
InterPro; IPR002917; MMR_HSR1.
Pfam; PF01018; GTP1_OBG; 1.
Pfam; PF01926; MMR_HSR1; 1.
PROSITE; PS00905; GTP1_OBG; 1.
Complete proteome.
SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTWOL8;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
45;
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                                                                                                                                                                                                                    57.9%; Score 44; DB
53.3%; Pred. No. 45;
ive 3; Mismatches
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01-DEC-2001 (TrBMBLrel. 19, Created)
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InterPro; IPR006074; GTP1/OBG dom.
InterPro; IPR006169; GTP1 OBG sub.
InterPro; IPR002917; WMR_HSR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 35:32-40(2003).
EMBL; BX640437; CAE30810.1; -.
HSSP; P44681; 1JAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00905; GTP1_OBG; 1.
                                                                                                                                                                                                                                                                                                                                                                  | |:|:| : ||||
356 EDPRFDASRGGAAPA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 EDERFDASRGGAAPA 370
                                                                                                                                                                                                                                                                                                                                   1 EKPKFEAYKAAAAPA 15
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NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                8; Conservative
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
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SEQUENCE 377 AA
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                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698; MEDLINE=21396508; Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Orhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;

"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

EMBL; AL591985; CAC49783.1; -.

InterPro; IPR009273; DUF930.

Pfam; PF06059; DUF930: 1.
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25-OCT-2004 (Rel. 45, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò.
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meningitidis Z2491.";
Nature 404:502-506(2000).
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP
diphosphate + L-tryptophanyl-tRNA(Trp).
diphosphate + L-tryptophanyl-tRNA(Trp).
Tryptophanyl-tRNA(Trp).
                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2; Length 306;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome; Hypothetical protein; Plasmid.
SEQUENCE 306 AA; 32638 MW; 01D9CC644001E67E CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein SMb20676.
                                                                                                                                    Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=trpS; OrderedLocusNames=NMA1682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|: ||:::|||||
66 RPQPEAFESAAAPA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KPKFEAYKAAAPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                    Plasmid
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
Dougherty B.A., Mason T.M., Clecko A., Parksey D.S., Blair E.,
Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Neisseria meningitidis serogroup B strain \mathsf{MC58}^{-1};
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09JY09;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                              HAMAP; MF 00140; -; 1.

InterPro; IPR002305; tRNA-synt_lb.

InterPro; IPR001412; tRNA-synt_l.

InterPro; IPR001306; Trp_tRNA-synt_lb.

Pfam; PF00579; tRNA-synt_lb; 1.

PRINTS; PR01039; TRNASYNTHTRP.

TIGRFAMS; TIGR00233; trpS; 1.

PROSITE; PS00178; AA TRNA_LIGASE I; FALSE NEG.

Aminoacyl-tRNA synthétase; ATP-binding; Complete protecome; Ligase; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-i- SUBUNIT: Homodimer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
NCBI TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 336; 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                     "HIGH" region.
"KMSKS" region.
ATP (By similarity).
3400C34F42E34536 CRC64;
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modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=trpS; OrderedLocusNames=NMB1471;
                                                                      EMBL; AL162756; CAB84910.1; -. PIR; E81863; E81863.
HSSP; P00953; 1MAU.
                                                                                                                                                                                                                                                                                                                                                                            37622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 ESPLFEIYKAFSTPS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EKPKFEAYKAAAAPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.6
Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                       203 2
206 2
336 AA;
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                            EMBL; AE002496; AAF41828.1; -...

R PIR; B81081; B81081.

R HSSP; P00953; 1MAU.

R TIGR; NMB1471; -...

R InterPro; IPR002305; tRNA-synt_1b.

R InterPro; IPR002306; Trp_tRNA-synt_1.

R InterPro; IPR002306; Trp_tRNA-synt_1.

R Pfam; PF00579; tRNA-synt_1b.

R Pfam; PF00579; tRNA-synt_1b.

R PROSITE; PS00178; AA_TRNA_LIGASE 1; FALSE_NEG.

M Aminoacy1-tRNA synthetase; ATP-binding; Complete proteome; Ligase;

M Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                     Query Match 56.6%; Score 43; DB 1; Length 336; Best Local Similarity 53.3%; Pred. No. 60; Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                  12 20 "HIGH" region.
203 207 "KMSKS" region.
206 206 ATP (By Bimilarity).
336 AA; 37616 MW; OAE32C8C00B621AA CRC64;
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Search completed: March 31, 2005, 02:41:11 Job time : 82.5645 secs

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Compugen Ltd.
version - 2005
GenCore
Copyright (c) 1993
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- protein search, using sw model OM protein

March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds (without alignments) 65.338 Million cell updates/sec Run on:

US-10-056-583A-95

1 EKAKFEAFKAAAAA 15 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

Database

A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2001s:*
5: geneseqp2001s:* geneseqp2003as:*geneseqp2003bs:*geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Abn52301	Abp52302	Abp52271	Abp52298	Abp52294	Abp52296	Abp52295	Abp52303	Abp52270	Abp52297	Abp52291	Abp52263	Abp52272	. Abp52259	Abp52257	Abp52300	Abp52304	Abp52299	Abp52253	Abp52251	Abp52239	Abp52290	Abp52261	Abp52244	Abp52292
SUMMAKIES	ABD50301	ABP52302	ABP52271	ABP52298	ABP52294	ABP52296	ABP52295	ABP52303	ABP52270	ABP52297	ABP52291	ABP52263	ABP52272 .	ABP52259	ABP52257	ABP52300	ABP52304	ABP52299	ABP52253	ABP52251	ABP52239	ABP52290	ABP52261	ABP52244	ABP52292
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Score	69		63	63	63	63	63	61	57	26	53	53	52	51	51	20	20	49	48	48	48	47	47	47	47
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HLA-DR2 m HLA-DR2 m HLA-DR3 m HLA-DR	Peptide w
Abp52269 Abp52264 Abp52264 Abp52265 Abp52280 Abp52289 Abp52305 Abp52289 Abp52305 Abp52289 Abp52305 Abp52289 Abp52305 Abp63276 Ad896704 Aay82058	Aag63198
ABP52269 ABP52262 ABP52264 ABP52267 ABP52265 ABP52254 ABP52254 ABP52254 ABP52240 ABP52249	AAG63198
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668 688 688 688 688 688 688 688 688 688	60
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ALIGNMENTS

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent. HLA-DR2 molecule binding peptide SEQ ID NO:95. ABP52301 standard; peptide; 15 AA (first entry) 16-OCT-2002 ABP52301; RESULT 1 ABP52301

Homo sapiens Synthetic.

WO200259143-A2.

01-AUG-2002.

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

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such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                 Sequence 15 AA;
                                                                                                                               invention
          8X8888X8
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Gaps ö Score 69; DB 5; Length 15; Pred. No. 0.00012; Mismatches 0; Indels 100.0%; Sc 100.0%; Pr tive 0; EKAKFEAFKAAAAA 15 Query Match Best Local Similarity 100. Matches 15; Conservative g ઠે

EKAKFEAFKAAAAA 15

ABP52302 standard; peptide; 17 AA ABP52302;

(first entry) 16-OCT-2002 HLA-DR2 molecule binding peptide SEQ ID NO:96.

Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent

Homo sapiens. Synthetic.

WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P

(HARD) HARVARD COLLEGE

Ξ Fridkis-Hareli Strominger JL,

WPI; 2002-608439/65

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MFC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to RESULT 2
ABP52302
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AC ABP5
XX
DT 16-0
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DE HLAXX
KW HUMA
KW HLAKW HLACO Synt
KW HLACO COMP
CC C

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Gaps
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                  Length 17;
                                     1; Indels
                 Score 64; DB 5; I
Pred. No. 0.00087;
0; Mismatches 1;
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0
                   92.8%;
                                        Conservative
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les 14; Conser
Sequence 17 AA;
                  Query Match
                                        Matches
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1 EKAKFEAFKAAAAA 15 EKAKFEAFKAAAAPA 17 g ð

RESULT

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ABP52271 standard; peptide; 15 AA ABP5227 ID AB

ABP52271;

(first entry) 16-OCT-2002

HLA-DR2 molecule binding peptide SEQ ID NO:65.

Human leukocyte antigen, HLA, major histocompatibility complex, MHC; HLA-DR2; MHC class II DR-2 molecule, demyelinating, multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;

anti-tumour necrosis factor agent

sapiens. Synthetic. WO200259143-A2

01-AUG-2002.

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Strominger JL, Fridkis-Hareli

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WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to The present invention describes compositions (I) comprising a peptide nvention

Sequence 15 AA;

Gaps .. 0 Score 63; DB 5; Length 15; Pred. No. 0.0011; 2; Mismatches 0; Indels 91.3%; Query Match
Best Local Similarity 80...
13; Conservative

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1 EKAKFEAFKAAAAA 15

HLA-DR2 molecule binding peptide SEQ ID NO:88.

(first entry)

16-OCT-2002

ABP52294;

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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                   HLA-DR2 molecule binding peptide SEQ ID NO:92.
                                          ABP52298 standard; peptide; 15 AA
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ABP 2298

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XX ABP 2298

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ABP 2298

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ABP 2298

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ABP 2298

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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                         Score 63; DB 5; Length 15; Pred. No. 0.0011; Mismatches 0; Indels
                          91.3%;
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EKAKYEAYKAAAAA 15
             Query Match
Best Local Similarity
13; Conservative
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ABP52294 standard; peptide; 17 AA.

RESULT 5
ABP52294
ID ABP5:

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New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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                                                                                                               Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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86.7%; Pred. No. 0.0013;
ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                        anti-tumour necrosis factor agent
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
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Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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                                                                                                                                                                                 anti-tumour necrosis factor agent
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86.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                      sapiens.
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                                                                                                                                                                                                                                                                   New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
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                                                                                                                                                                                                                                                                                                                                                                                    peptide
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Pred. No. 0.0014;
2; Mismatches 0; Indels
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                                                                                                           24-JAN-2002; 2002WO-US002071.
                                                                                                                                          24-JAN-2001; 2001US-0263569P.
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                          encephalomyelitis.
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              Synthetic.
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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Pred. No. 0.0027;
1; Mismatches 1; Indels
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                                                                                                                                                                                          Fridkis-Hareli M;
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                                                                 24-JAN-2001; 2001US-0263569P.
  24-JAN-2002; 2002WO-US002071
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ABP52270
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AC ABP5
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DB HLA--
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                                            New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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Pred. No. 0.011;
7; Mismatches
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                                                                                                                                    Claim 28; Page 39; 54pp; English.
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EAAKYEAYKAAAAAA 15
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Best Local Similarity 80.0
Matches 12; Conservative
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                  WPI; 2002-608439/65.
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Sequence 15 AA;
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to Claim 28; Page 39; 54pp; English

1 EKAKFEAFKAAAAA 15 Local Similarity 80.0 Query Match Matches

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2; Indels

81.2%; Score 56; DB 5; Length 15; 80.0%; Pred. No. 0.016;

1; Mismatches

ABP52291 standard; peptide; 15

EKPKFEAYKAAAAPA 15

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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; HLA-DR2 molecule binding peptide SEQ ID NO:85. anti-tumour necrosis factor agent. (first entry) 16-OCT-2002 ABP52291;

WO200259143-A2 sapiens. 01-AUG-2002 Synthetic. Ношо

24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Fridkis-Hareli WPI; 2002-608439/65 Strominger JL,

New compositions comprising synthetic peptides in complex with a major. histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP55207 to New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis. ô immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; Gaps ő 76.8%; Score 53; DB 5; Length 15; 73.3%; Pred. No. 0.049; ive 2; Mismatches 2; Indels HLA-DR2 molecule binding peptide SEQ ID NO:57. Example 1; Page 33; 54pp; English. ABP52263 standard; peptide; 15 AA. anti-tumour necrosis factor agent Σ Fridkis-Hareli 24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P. 1 EKAKFEAFKAAAAA 15 (first entry) 11; Conservative (HARD) HARVARD COLLEGE WPI; 2002-608439/65. Similarity WO200259143-A2. Strominger JL, Sequence 15 AA; 16-OCT-2002 01-AUG-2002 Synthetic Query Match Best Local S Matches ABP52263 8 $\frac{1}{2}$ $\frac{1}{2}$ g 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52205 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
ABP52305 represent peptides used in the exemplification of the present
                                                                                                                      Gaps
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                                                                                  Score 53; DB 5; Length 15;
Pred. No. 0.049;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                 HLA-DR2 molecule binding peptide SEQ ID NO:66.
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                                                                                                                                                                                                                                                                           ABP52272 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fridkis-Hareli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-2002; 2002WO-US002071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-2001; 2001US-0263569P.
                                                                                   76.88;
                                                                                                    73.3%;
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EEAKYAAYKAAAAAA 15
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                                                                                                                     11; Conservative
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                                                                                                    Local Similarity
                                                   Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200259143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strominger JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                             ABP52272;
                                                                                   Query Match
                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                          RESULT 13
ABP52272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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Score 52; DB 5; Length 15; Pred. No. 0.072;

75.4%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                                                                                                                                                                                                                       ABP52259 standard; peptide; 15 AA.
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1 EAKKYEAYKAAAAA
EKAKFEAFKAAAAA
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Matches 11; Conserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strominger JL,
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                              Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                                                                                                                                             HLA-DR2 molecule binding peptide SEQ ID NO:51.
                                      ABP52257 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 32; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-2001; 2001US-0263569P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002; 2002WO-US002071
                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strominger JL,
                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                            16-OCT-2002
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                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                         ABP52257;
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RESULT 15
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. 0 Gaps ő Score 51; DB 5; Length 15; Pred. No. 0.11; 2; Mismatches 2; Indels 73.9%; Local Similarity 73.3%; les 11; Conservative 5 Query Match Best Loca Matches

1 EKAKFEAFKAAAAA 15

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| ||: |:||||||| EAAKYAAYKAAAAAA 15

Search completed: March 31, 2005, 02:35:28 Job time : 88.7903 secs

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5.1.6
Compugen Ltd.
 GenCore version Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds (without alignments)
48.718 Million cell updates/sec Run on:

US-10-056-583A-95 69 1 EKAKFEAFKAAAAA 15 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

513545 seqs, 74649064 residues Searched:

513545 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
7. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 18658, A	221	135		Ġ	9	4	Sequence 16, Appl	~	S	7		950,	7747,	4241	33, AI	30,	1445	. 52739	Patent No. 5482709	Patent No. 5273901	Patent No. 5482709	Sequence 4239, Ap	10	5,	7,	7,
	ID	US-09-248-796A-18658	US-09-252-991A-22139	US-09-489-039A-13950	PCT-US95-04121-38	US-08-295-670-6	US-08-633-485-6		09-117-	US-09-117-121-24	US-09-344-529-5	09-248	G)	n	-681A-77	US-09-328-352-4241	PCT-US94-10257A-33	US-09-117-121-30	US-09-732-210-1445	5273901-7	5482709-6	5273901-7	5482709-6	US-09-328-352-4239	US-09-919-497-100	US-09-060-450-5	US-09-405-743A-7	US-09-816-989A-7
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*	Match	58.0	56.5	56.5	55.1	55.1	S	55.1	53.6	53.6	53.6	•		53.6		•	•	•	52.2		•			52.2			50.7	50.7
	Score	40				38	38	38	37	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	35	35	35
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5527, Ap 11599, A 16623, A 3759, Ap 4, Appli 7, Appli 7, Appli 7, Appli	26859, A 20, Appl 7165, Ap	6873, Ap 8171, Ap 26, Appl		1, Appli
Sequence 5527, Ap Sequence 11599, A Sequence 16623, A Sequence 3759, Ap Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
US-09-513-999C-5527 US-09-902-540-11599 US-09-902-540-16623 US-09-134-000C-3759 US-07-637-870-4 US-07-640-476-7 US-07-640-476-7	US-09-252-991A-26859 US-09-134-078-20 US-09-949-016-7165	US-09-543-681A-6873 US-09-489-039A-8171 US-09-673-198-26	US-09-198-452A-171 US-09-438-185A-152 US-09-345-473E-40	US-09-411-578-1
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ALIGNMENTS

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APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (21)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-18658
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                 Sequence 18658, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: UNSURE
US-09-248-796A-18658
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818 KAKEEAEAAAAAA 831 2 KAKFEAFKAAAAA 15 g ਨੇ

Sequence 21139, Application US/09252991A

Facent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27 RESULT 2 US-09-252-991A-22139

us-10-056-583a-95.rai

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Gaps
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                                                                                                                                                                        Length 13;
                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESS...
STREET: 1755 S. Jeilelson.
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,670
FILING DATE: 13-AN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00039
FILING DATE: 13-JAN-1993
ATPORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5547864man F.
REGISTRANCE/DOCKET NUMBER: 10-697-0 PCT
TELEPHONE: (703) 413-2220
TELEFRANCE (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08295670
; Patent No. 5547864
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, HISASHI
; APPLICANT: TSUCHIYA, MAKOTO
; APPLICANT: KAWAHARA, YOSHIO
; TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1;
Pred. No. 1.6e+02;
3; Mismatches 4
                                                                                                                                                                        Score 38; DB 5;
Pred. No. 4.6;
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                                                                                                                                                                          55.1%;
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Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                              | ::| |||||||
1 AAYKAAKAAAAA 13
           13 amino acids
                                                                                                                                                                   Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US95-04121-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-295-670-6
                             TYPE: amino acid STRANDEDNESS:
                                                                       linear
                                                                     ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                             Sequence 13950, Application US/09489039A
Sequence 13950, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13950
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                                                                                                                                               Score 39; DB 4; Length 166; Pred. No. 39; 3; Indels 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 4; Length 466; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Haptenated Peptides and Uses Thereof NUMBER OF SEQUENCES: 62
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin PC-Base #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04121
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1e+02;
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REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 079.2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application PC/TUS9504121 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,206
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
                                                              ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%;
                                                                                                                                              Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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104 KAQVDAFHAAALAA 117
                                                                                                                                                                                                                             2 KAKFEAFKAAAAA 15
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Matches 10, Conservative
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NUMBER OF SEQ ID NOS:
SEQ ID NO 22139
LENGTH: 166
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PCT-US95-04121-38
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ZIP:: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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104 EQAAYEAFEAARVRA 118
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         Renaud, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-508-7618-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-117-121-16
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0
                                                                                                                                                                                            APPLICANT: KAWASAHI, HISASHI
APPLICANT: KAWASAHI, HISASHI
APPLICANT: TSUCHIYA, NAKOTO
APPLICANT: TSUCHIYA, NAKOTO
APPLICANT: TSUCHIYA, NAKOTO
APPLICANT: MARAHARA, YOSHIO
TTILE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
MUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
COUWRRY: U.S.A.
ZIP: 22202
ZIP
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Patent No. 6027920
GENERAL INFORMATION:
APPLICANT: Joliff, Gwennael
APPLICANT: Guyonvarch, Armel
APPLICANT: Purification, Relano
APPLICANT: Duchiron, Francis
                                                                                                                   US-08-633-485-6
; Sequence 6, Application US/08633485
; Patent No. 5681717
  104 EQAAYEAFEAARVRA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 497 amino acids
amino acid
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Best Local Similarity 53.3.
Lan 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-633-485-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-508-761B-4
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Gaps
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Patent No. 6307020

GENERAL INFORMATION:

APPLICANT: Hew, Choy

APPLICANT: Gong, Zhiyuan

TITLE OF INVENTION: and Nucleic Acids

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE:..California

COUNTRY: USA
                     System for Protein Expression and
Secretion Especially in Corynebacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 510;
APPLICANT: Kenaud, mached TITLE OF INVENTION: System for Protein Expression and TITLE OF INVENTION: Serretion Especially in Corynebact(NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Jacobson, Price, Holman & Stern, PLLC STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: US/08/509,761B
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
FILING DATE: 02-AUG-1991
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: PR 91/09670
FILING DATE: 02-AUG-1991
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: PS9525NA
TELEPHONE: (202) 393-5350
TELEPHONE: (202) 393-5350
INFORMATION FOR SEQ ID NO: 4:
CENTING FOR SEQ ID NO: 4:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.1%; Score 38; DB 3; 1 Best Local Similarity 53.3%; Pred. No. 1.7e+02; Matches 8; Conservative 3; Mismatches 4.
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2 KAKFEAFKAAAAA 15
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                            Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
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US-09-248-796A-25516
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Batent No. 6307020

GENERAL INFORMATION:

APPLICANT: Hew, Choy

TITLE OF INVENTION: Intracellular Antifreeze Polypeptides

TITLE OF INVENTION: and Nucleic Acids

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STREET: Contraction

ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 3; Length 38;
Pred. No. 19;
0; Mismatches 4; Indels
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ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/117,121

FILING DATE: 20-NOV-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/CA97/00062

FILING DATE: 30-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 016252-001610US

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/CA97/00062

FILING DATE: 30-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

TELEPOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: (415) 576-0200

TELEPAX: (415) 576-0200

TELEPAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-117-121-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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, 53.6%; Score 37; DB 3; Length 38;

Query Match

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Sequence 25516, Application US/09248796A

Sequence 25516, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 25516

LENGTH: 69
                                                                                                                                                                                                         USCOURT 14-529-5
; Sequence 5, Application US/09344529
; Sequence 5, Application US/09344529
; Patent No. 6429293
; GENERAL INFORMATION:
; APPLICANT: Hew, Choy L.
; APPLICANT: HSC Research and Development Limited Partnership
; TITLE OF INVENTION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
; FILE REFERENCE: 016252-002620US
; CURRENT APPLICATION NUMBER: US 60/090,794
; EARLIER APPLICATION NUMBER: US 60/090,794
; EARLIER APPLICATION NUMBER: US 60/095,713
; ARLIER PILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 38
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                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pleuronectes americanus FEATURE: OTHER INFORMATION: Winter flounder skin-type antifreeze polypeptide OTHER INFORMATION: (wfsAFP-1)
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                         Indels
                         4 ;
Pred. No. 19;
0; Mismatches
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Best Local Similarity 71.4%;
Matches 10; Conservative
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us-10-056-583a-95.rai

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                             Sequence 1021, Application US/09198452A;
Sequence 1021, Application US/09198452A;
GENERAL INFORMATION:
FAPPLICANT: Griffals, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever ITILE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A;
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-543-681A-7747

; Sequence 7747, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Sequence 950, Application US/09438185A

Patent No. 6822071

GENERAL INFORMATION:

APPLICANT: Mitchell, Wayne

APPLICANT: Mitchell, Wayne

APPLICANT: Kalman, Sue

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

TITLE REFERENCE: 018941-000411US

CURRENT APPLICATION NUMBER: US/09/438,185A

CURRENT FILING DATE: 1998-11-12

PRIOR FILING DATE: 1998-11-12

PRIOR FILING: DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 1074

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 37; DB 4; Length 479; 72.7%; Pred. No. 2.3e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            53.6%; Score 37; DB 4; Length 476; 72.7%; Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: CPn0948
US-09-438-185A-950
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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107 RFSAFAAAAA 117
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110 RFSAFAAAAA 120
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RESULT 12
US-09-198-452A-1021
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US-09-438-185A-950
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Sequence 4241, Application US/09328352

Batent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF TOWNERTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF TOWNERNIES: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4241
LENGTH: 759
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         DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 4; Dred. No. 3.6e+02; O; Mismatches 4
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEU; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7747
; LENGTH: 576
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Job time : 23.9839 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
US-09-328-352-4241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.6%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           444 KAKEEQAKAAAKAA 457
                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-328-352-4241
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Thu Mar 31 14:05:36 2005

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds (without alignments)
74.648 Million cell updates/sec

US-10-056-583A-95 69

1 EKAKFEAFKAAAAA 15 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

.1407402 seqs, 331100923 residues Searched:

1407402 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

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cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* Published Applications AA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

18: 19: 20:

SUMMARIES

	 Appl	App1	Appl	App]	Appl	Appl	App1	Appl	App1	App1	Appl	App1	App1
	. , 56	96	65,	88,	90,	89,	97,	64,	-	91,	57,	35,	. ,99
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence
ΩI	US-10-056-583-95	US-10-056-583-96	US-10-056-583-65	US-10-056-583-88	US-10-056-583-90	US-10-056-583-89	US-10-056-583-97	US-10-056-583-64	US-10-056-583-92	US-10-056-583-91	US-10-056-583-57	US-10-056-583-85	US-10-056-583-66
DB	14	14	14	14	14	14	14	14	14	14	14	14	14
% Query Match Length DB	15	17	15	17	17	19	17	15	15	15	15	15	15
% Query Match	100.0	92.8	91.3	91.3	91.3	91.3	88.4	82.6	82.6	81.2	76.8	76.8	75.4
Score	69	64	63	63	63	63	61	57	57	26	53	53	25
Result No.	-	7	m	4	5	9	7	80	90	10	11	12	13

Appl		4, Appl	_				_			_	_	_	_	_	_	_		_	_	_	_		_	_	_	Appl ,	41270,	141271,	Appl	•	, Appl
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US-10-056-583-51	-10-056-5	10-056-	-10-056-583-9	10-056-583-9	10-056-58	10-056-583-4	10-056-583-4	10-056-583-3	US-10-056-583-55	0-056-583-5	0-056-58	0-056-583-8	-056-583-8	0-056-583-	0-056-58	0-056-583-	0-056-58	10-056-	-056-58	0-056-583-3	-056-5	-10-056-583-4	56-583-4	56-583-4	26-5	-58	US-10-437-963-141270	_	US-09-765-301-24	9-165-6	US-10-056-583-25
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	16	16	σ	10	14
15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	66	142	15	15	15
73.9	73.9	72.5	72.5	71.0	9.69	9.69	9.69	68.1	68.1	68.1	68.1	68.1	68.1	66.7	66.7	66.7	63.8	63.8	63.8	62.3	62.3	62.3	62.3	62.3	62.3	62.3	62.3	62.3	6.09	6.09	6.09
51	51	20	20	49	48	48	48	47	47	47	47	47	47	46	46	46	44	44	44	43	43	43	43	43	43	43	43	43	42	42	42
14	15	16	17	18	19	20	21	22	23	24	25	5 6	27	28		30			33	34	35	36	37		39	40	41	42	43	44	45

ALIGNMENTS

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0
               Sequence 95, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-581-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
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100.0%; Pred. No. 5.5e-05;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 15; Conservative
US-10-056-583-95
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Indels 1 EKAKFEAFKAAAAA 15 1 BKAKFEAFKAAAAA 15 ð ద

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Gaps

RESULT 2 US-10-056-583-96

us-10-056-583a-95.rapb

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APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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                                                              JENGERAL INFORMATION:

JENERAL INFORMATION:

JETE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR PILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 96

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.8%; Score 64; DB 14; Length 17;
93.3%; Pred. No. 0.00043;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%; Score 63; DB 14; Length 15;
86.7%; Pred. No. 0.00055;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Presidents and Fellows of Harvard College APPLICANT: Strominger, Jack L. APPLICANT: Strominger, Jack L. APPLICANT: Fridkis-Hareli, Masha TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING TITLE OF INVENTION: CONDITIONS FILE REFERENCE: 24655-017 CURRENT APPLICATION NUMBER: US/10/056,583 CURRENT FILING DATE: 2002-01-24 PRIOR APPLICATION NUMBER: 60/263,569 PRIOR FILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 88, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 65, Application US/10056583; Publication No. US20030064915A1; GENERAL INFORMATION:
Sequence 96, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 13; Conserv
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US-10-056-583-88
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Sequence 90, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

ITILE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 17

TENGTH: 17
                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 91.3%; Score 63; DB 14; Length 17; Best Local Similarity 86.7%; Pred. No. 0.00063; Matches 13; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 91.3%; Score 63; DB 14; Length 17; Best Local Similarity 86.7%; Pred. No. 0.00063; Matches 13; Conservative 2; Mismatches 0; Indels
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APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
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Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
FILE REFERENCE: 24655-007

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 88

LENGTH: 17
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
        SEQ ID NO 64
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Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT PILING DATE: 2002-01-24

CURRENT FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                 ; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-97
                                                                                                                                                                                                                                                                                 Query Match 91.3%; Score 63; DB 14; Length 19;
Best Local Similarity 86.7%; Pred. No. 0.00071;
Matches 13; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61; DB 14; Length 17;
Pred. No. 0.0014;
1; Mismatches 1; Indels
                                                            NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 89
LENGTH: 19
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 86.77
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-10-056-583-97
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; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Presidents and Fellows of Harvard College;
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR APPLICATION NUMBER: 60/263,569
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92
LENGTH: 15
TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                                         Score 57; DB 14; Length 15;
Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.6%; Score 57; DB 14; Length 15; 86.7%; Pred. No. 0.0056; 1; Mismatches 1; Indels
                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
                                                                                                                                                         82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                          1 EKAKFEAFKAAAAA 15
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1 EKAKEEAYKAAAAA 15
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                                                                                                                                                    Query Match
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 86.7
Matches 13; Conservative
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US-10-056-583-66

Sequence 66, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 66

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.4%; Score 52; DB 14; Length 15; Best Local Similarity 73.3%; Pred. No. 0.038; Matches 11; Conservative 2; Mismatches 2; Indels
          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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1 EKPKYEAYKAAAAPA 15
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1 EAKKYEAYKAAAAA 15
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          11; Conservative
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Best Local Similarity 73.3
Matches 11, Conservative
       Matches
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US-10-056-583-85

i Sequence 85, Application US/10056583

i Publication No. US20030064915A1

i GENERAL INFORMATION:

APPLICANT: Bresidents and Fellows of Harvard College

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 85

LENGTH: 15
                                                                                                                                                                                                                                                              RESULT 11
US-10-056-583-57

Sequence 57, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Strominger, Jack L.

APPLICANT: TILE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: 60/263,569

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 57

LENGTH: DEM
; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-57
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CTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85
                                                                   Score 56; DB 14; Length 15;
Pred. No. 0.0082;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.8%; Score 53; DB 14; Length 15; Best Local Similarity 73.3%; Pred. No. 0.026; Matches 11; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 14; Length 15; Pred. No. 0.026;
                                                                     81.2%;
80.0%;
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ORGANISM: Artificial Sequence
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EEAKYAAYKAAAAAA 15
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                                             Query Match
Best Local Similarity 80.07
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Best Local Similarity
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RESULT 14
US-10-056-583-51
Sequence 51, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
ITTLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT APPLICATION NUMBER: 60/263,569
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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1 EAAKYAAYKAAAAA 15
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RESULT 15
US-10-056-583-53
; Sequence 53, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2001-01-24
; PRIOR PILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.9%; Score 51; DB 14; Length 15; Best Local Similarity 73.3%; Pred. No. 0.056; Matches 11; Conservative 2; Mismatches 2; Indels
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1 EKAKFEAFKAAAAA 15 Q ⋧

Search completed: March 31, 2005, 02:48:49 Job time : 67.5323 secs

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Run on:

March 31, 2005, 02:26:17; Search time 17.9032 Seconds (without alignments) 80.614 Million cell updates/sec

US-10-056-583A-95 69 Title: Perfect score:

1 EKAKFEAFKAAAAA 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		من			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	47.5	68.8	189	5	S77930	exoskeletal protei
7	47.5	68.8	189	N	877935	exoskeletal protei
М	42	6.09	179	N	F97683	50S ribosomal prot
4	42	6.09	179	7	AF2908	50S ribosomal prot
ß	41	œ.	346	~	C82156	О
9	41	59.4	828	N	F96535	hypothetical prote
7	40	58.0	~	7	S04675	H+-transporting tw
80		58.0	869	7	T32594	hypothetical prote
თ	39	56.5	73	7	840015	
10	39	56.5	113	7	T30041	щ
11	39	56.5	144	~	D83152	
12	39	56.5	198	~	AI2622	- 124
13	39	56.5	217	7	A97405	hypothetical prote
14	39	56.5	250	~	T51971	
15	39	56.5	389	~	G87332	hypothetical prote
16	39	56.5	421	7	JV0057	
17	39	56.5	2957	~	T33152	hypothetical prote
18	38	55.1	151	-	GGICEH	globin CTT-VIII -
19	38	55.1	246	~	B72728	probable ribosomal
20	38	55.1	320	~	S76422	hypothetical prote
21	38	55.1	436	~	T31902	
22	38	55.1	510	~	S35028	-
23	38	55.1	525	-	QQBE6	BFLF1 protein - hu
24	37	53.6	231	7	T02585	
25	37	53.6	254	7	H86355	
56	37	53.6	270	~	G82108	
27	37	٠	359	7	H95865	₩.
	37	س	476	7	~	glycogen synthase
29	37	53.6	476	7	B86609	glycogen synthase

phosphoenolpyruvat	cell division cont	translation initia	transitional endop	hypothetical prote	165K protein, skel	probable rpsP prot	ribosomal protein	translation elonga	1-acylglycerol-3-p	hypothetical prote	hypothetical prote	ribosomal protein	hypothetical prote	hypothetical prote	phthalate dioxygen
AC0364	F75154	E64114	D75046	T34516	S43529	H70927	B87702	S43445	C70521	T51010	T51011	R5DOP0	C70410	B86255	A44230
N	N	~	~	0	~	~	7	~	7	~	~	Н	0	~	0
575	795	829	840	1430	1465	162	165	206	251	273	287	305	306	320	321
53.6	53.6	53.6	53.6	53.6	53.6	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2
37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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exoskeletal protein HACP202A - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77930
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
A;Description: Characterization of exoskeletal proteins from the American lobster, Homax A;Beference number: S77925
A;Accession: S77930
A;Accession: S77930
A;Accession: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                    Length 189;
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                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Best Local Simi]
Matches 12; (
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|||: |:||||| ||| 11 EKARFFQAFKAAEAAA 26 qq

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S77935
exoskeletal protein HACP202B - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77935
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homax A;Reference number: S77925
A;Accession: S77935
                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-189 <NOU>
A,Cross-references: UNIPROT:Q7M495
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Gaps 1; Length 189; 1; Indels . 7 Query Match 68.8%; Score 47.5; DB Best Local Similarity 75.0%; Pred. No. 1.3; Matches 12; Conservative 2; Mismatches 1 EKAK-FEAFKAAAAA 15 8

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RESULT 3 F97683

NID:99656310; PIDN:AAF94940

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Gaps

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C; Accession: F96535
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-828 <STO>
A,Cross-references: UNIPROT:Q9C6C7; GB:AE005173; NID:g10092168; PIDN:AAG12588.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-478 <TYB>
A;Cross-references: UNIPROT:P05440
C;Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase all
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding;
F;155-162/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Rhodopseudomonas blastica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Rhodopseudomonas blastica
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C; Accession: S04675
R; Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A; Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription. A; Reference number: S04666; MUID:85058188; PMID:6209404
A; Accession: S04675
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F10F5.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                  A;Residues: 1-346 <HEI>
A;Cross-references: UNIPROT:Q9KR55; GB:AE004256; GB:AE003852; NID:g
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1791
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2; Length 346;
Pred. No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 828;
                                      A; Reference number: A82035; MUID: 20406833; PMID: 10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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Pred. No. 56;
2; Mismatches
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90.0%;
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EKAAVEAFEAASA 170
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les 9; Conserv
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Best Local Similarity
Matches 9; Conserv
                                                                                                                  A, Status: preliminary A; Molecule type: DNA
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Best Local S:
Matches 9
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50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: F97683
R; Goodner: F; Wollam, C; Allinger, M; Doughty, D; Scott, C; Lappas, C; Markelz, B;
Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A; Accession: F97683
A; Accession: F97683
A; Accession: F97683
A; Accession: F97683
A; Mullinary
A; Molecule type: DNA
A; Molecule type: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C; Accession: AF2908 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
C82156
conserved hypothetical protein VC1791 [imported] - Vibrio cholerae (strain N16961 serogr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82156
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
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A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19
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137 EKARLEAEKVAAAQA 151
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137 EKARLEAEKVAAAQA 151
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Best Local Similarity 66.7
Matches 10; Conservative
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A,Status: preliminary
A,Molecule type: DNA
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Gaps

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14:05:36 2005

Thu Mar 31

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A;Cross-references: UNIPROT:Q19615; EMBL:U53150; PIDN:AAA96131.1; GSPDB:GN00023; CESP:F2
A;Experimental source: strain Bristol N2; clone F20A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PA3956 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: DS-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83152
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9HX60; GB:AE004813; GB:AE004091; NID:g9950134; PIDN:AAG0734
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein Atu0377 [imported] - Agrobacterium tumefaciens (strain C5 conserved hypothetical protein Atu0377 [imported] - Agrobacterium tumefaciens (strain C5 C; Species: Agrobacterium tumefaciens (c) Species: Agrobacterium tumefaciens (c) Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C; Accession: AI2622 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
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                                                                                          C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T30041
R.Gattung, S.; Wu, X.
submitted to the EMBL Data Library, March 1996
A.Description: The sequence of C. elegans cosmid F20A1.
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A;Introns: 22/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F57E7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 68.8%; Pred. No. 19; Conservative 1; Mismatches 2; Indels
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                                                                - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
A;Residues: 1-113 <GAT>
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Pred. No. 24;
2; Mismatches
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Best Local Similarity 64.3%;
Matches 9; Conservative
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82 KAQVDAFHAAALAA 95
                                                                   hypothetical protein F20Al.1
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Best Local Similarity (
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A;Molecule type: DNA
A;Residues: 1-144 <STO>
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C;Genetics:
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840015
pdd protein - phage P1
C; Species: phage P1
C; Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C; Accession: 840015; S38533
R; Lehnherr, H.; Maguin, E.; Jafri, S.; Yarmolinsky, M.B.
J. Mol. Biol. 233, 414-428, 1993
A; Title: Plasmid addiction genes of bacteriophage P1: doc, which causes cell death on cu A; Reference number: 840015; MUID: 94016561; PMID: 8411153
A; Molecule type: DNA
A; Residues: 1-73 < LEH>
A; Residues: 1-73 < LEH>
A; Residues: 1-73 < LEH>
A; Cossarreferences: UNIPROT: Q06253; GB: M95666; NID: 9463276; PIDN: AAa16932.1; PID: 9215645
B; Schmidt, C.; Lehnherr, H.; Guidolin, A.; Arber, W.
submitted to the EMBL Data Library, November: 1992
A; Description: Additional late promoter sequences of bacteriophage P1.
A; Reference number: 838553
A; Molecule type: DNA
A; Residues: 1-73 < SCH>
A; Residues: 1-73 < SCH>
A; Residues: 1-73 < SCH>
A; Cross-references: EMBL: M95666; NID: 9463276; PIDN: AAA16932.1; PID: 9215645
                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C02B10.5 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C; Accession: T32594
R; Melson, J; White, S; Hawkins, J; Wohldmann, P.
Submitted to the EMBL Data Library, December 1997
A; Description: The sequence of C. elegans cosmid C02B10.
A; Reference number: Z21196
A; Reference number: Z21196
A; Reservation: T32594
A; Residues: Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-698 «NEL>
A; Residues: 1-698 «NEL>
A; Residues: 1-698 «NEL>
A; Residues: 1-698 «NEL>
A; Residues: Cosmid Source: strain Bristol N2; clone C02B10
C; Genetics:
A; Gene: CESP: C02B10.5
A; Map position: 4
A; Introns: 61/3; 102/2; 188/3; 349/2; 641/1
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F;181-357/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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                                                                                                                              3; Indels
                                                           Query Match 58.0%; Score 40; DB 2; Best Local Similarity 66.7%; Pred. No. 49; Matches 10; Conservative 2; Mismatches 3
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464 EEAKAKAAKLAAAAA 478
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Best Local Similarity
Matches 9; Conserv
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A; Gene: CC0674
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A; Title: The comper: AB25//; colored http://www.nater.colored http://wwww.nater.colored http://www.nater.colored http://www.nater.colored http://
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A97405
hypothetical protein AGR_C_660 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C; Species: Agrobacterium tumefaciens
C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: A97405
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KUR>
A;Cross-references: UNIPROT:Q8UICO; GB:AE007869; PIDN:AAK86194.1; PID:g15155291; GSPDB:G
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N;Alternate names: 20S proteasome chain PAD2
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
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A;Title: Molecular organization of the 20S proteasome gene family from A;Reference number: Z25275; MUID:9611183; PMID:9611183
A;Accession: T51971
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A;Experimental source: strain Columbia; seedling hypocotyls
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-250 <FUH>
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Pred. No. 35;
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A; Map positIon: circular chromosome
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Best Local Similarity 80.0%;
Matches 8; Conservative
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95 KAKMEAFRAA 104
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114 KAKMEAFRAA 123
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56.5%; Score 39; DB 2; Length 250;

Query Match

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C; Species: Caulobacter crescentus
C; Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: G87332
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: 09AAC8; GB: AE005673; NID: 913421893; PIDN: AAK22659.1; GSPDB:G
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60;
                                   Indels
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Pred. No. 60;
0; Mismatches
      Pred. No. 40;
0; Mismatches
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Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.5%;
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                230 AKIBABKAAABAA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 KTSVETFKAAAAPA 79
                                                                              3 AKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-389 <STO>
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us-10-056-583a-95.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds
 (without alignments)
95.342 Million cell updates/sec

1 EKAKFEAFKAAAAA 15 US-10-056-583A-95 69 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	95 homarus ame	96 homarus ame	p3 uncultured	ts oryza sativ				'n	œ	_		_		_	55 vibrio chol					sl oryza sativ		v2 plasmodium	_	₩.	m						60 pseudomonas
		Desc	Q7m495	Q7m496	Q64cp3	Qeert	P5088	Q9uan1	09213	Ognpz Ognpz	P5816	06uk8	Q6w18	Q6d7£3	Q6qut	07 q1q4	Q9kr55	Q98kc4	09c6c7	Q6ft73	Q650y0	Q6yw 81	P054	Q64jv2	04444	Q86a1	06555	Q77cd4	Q84w05	006253	Q79a04	019615	Q9hx60
SUMMARIES		I ID	Q7M495	Q7M496		QGERTS			RL19_RHIME		RL19		_	_	_	01010	_		_		-	_		_		_			_		_	_	O9XH6O
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		Match Length	189	189	707	66	299	312	177	179	181	274	386	395							369		47				3247	ന					144
	Query	Match	68.8	68.8	3	N	62.3	62.3	6.09	6.09	6.09	6.09	6.09	60.9	60.9	59.4	59.4	59.4	59.4	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	56.5	56.5	56.5	56.5	56.5
		Score	47.5	47.5	44	43	43	43	42	42	42	42	42	42	. 42	41	41	41	41	40	40	40	40	40	40	40	40	40	39	39	39	39	39
	Result	NO.	H	7	m	4	ហ	9	7	60	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31

Q7y3m5 enterobacte	Q7xvt5 oryza sativ		Q7w769 bordetella	-			Q72cn6 desulfovibr	Q67ps1 symbiobacte	_		Q62176 burkholderi	щ	Q65wf6 mannheimia
Q7Y3M5	Q7XVT5	QBUICO	Q7W769	Q7D1K6	Q7WIK3	PS72 ARATH	Q72CN6	Q67PS1	Q9VFL4	Q9XZR1	Q62L76	Q63V82	Q65WF6
8	~	N	~	N	7	Ч	0	~	0	7	~	0	7
145	153	198	199	217	219	250	273	292	300	327	342	342	376
56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5
39	39	39	39	33	39	39	39	39	39	39	39	39	39
32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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H
                                                                                                                                                           777495 PRELIMINARY; PRT; 189 AA.
C Q7M495;
C Q7M495;
T 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
T 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
T 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
E Exoskeletal protein HACP202B (Fragment).
S Homarus americanus (American lobster).
C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Homarus.
                                                                                                                                                                                                                                                                          68.8%; Score 47.5; DB 2; Length 189; 75.0%; Pred. No. 6.2; iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0 Matches 12; Conservative
RESULT 1
Q7M495
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1 EKAK-FEAFKAAAAA 15 |||: |:||||| ||| 11 EKARFFQAFKAAEAAA 26 g ð

RESULT 2

Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.; Submitted (JUN-1997) to the PIR data bank.
PIR; S77930; S77930.
NON_TER 1 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exoskeletal protein HACP202A (Fragment).
Homarus americanus (American lobster).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Homarus. 189 AA; 20154 MW; 72A4EFCD9C647FE9 CRC64; 189 AA. PRT; PRELIMINARY; NON TER SEQUENCE SEQUENCE Q7M496 Q7M496; 27M496 STIRE REPRESENTATION OF THE PROPERTY OF THE PR

68.8%; Score 47.5; DB 2; Length 189;

Query Match

d 8

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Gaps

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RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Li P.W., Bans C.A., Goosyne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA, Burton G.G., Worttman J.R., Yandell M.D., Zhang O., Chen L.X., Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA, Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA, Bril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA, Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Belos D.V., Bernam B.P., Bhandari D., Bolshakov S., RA, Berkova D.W., Bouch H., Cavley S., Dulke C., Davenport L.B., Center A., Chandra I., Ra Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Pleischmann W., Roboson K.J., Bough L.B., Downes M., Digar Rocha S., Durkov B.C., Dunn P., RA, Borlow B., Dowler M., Digar R.A., Goorg F., Gonrer M., Digar R., Herman R.S., Galbart W.M., Glasser K., Rosin D. Houston K.A., Howland T.J., Wei Mer., Houck J., Houston K.A., Howland T.J., Wei Mer., Merherson D., Merkilov G., Milshina N.V., Mozleod M.P., Mcheofon D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Alandar M., Stupski M.P., Sanih T., Shue B., McInton K.A., Misch M.-H., Degwar M., Mohnt S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L., Reinert K., Remington K., Stupskern D.K., Warskern D.R., Park S., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sanih T., Shue B., Williams S.M., Woodage T., Worley S., Zhan M., Zhan G., Zhan M., Zhan G., Zhan M., Zhan G., Zhan M., Zhan G., Zhan K., 
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
                                                                                                                                                                                                                                                                    D RL22 DROME STANDARD; PRT; 299 AA.

PR0-07-1996 (Rel. 34, Created)

1 01-07-1996 (Rel. 34, Last sequence update)

1 01-NOV-1997 (Rel. 35, Last sequence update)

25-JAN-2005 (Rel. 46, Last annotation update)

E 60S ribosomal protein L22.

Name=RpL22; ORFNames=CG7434;

Drosophila melanogaster (Fruit fly).

E bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glover C.V.C., Bidwai A.P., Zhao W.F.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.";
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                             66.7%; Pred. No. 19;
tive 1; Mismatches
                                                                                                        1 EKAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibbs R.A., Myers E.W., Rub
"The genome sequence of Dro
Science 287:2185-2195(2000)
                               Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                        81 ERLSFLLFKAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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DROME
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                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reverse methanogenesis: testing the hypothesis with environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                      1;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.8%; Score 44; DB 2; Length 707; 73.3%; Pred. No. 79; 3; Indels
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Putnam N., Detter J.C., Richardson P.M., Rokhsar D.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY714833; AAU82834.1; -.
Hypothetical protein.
SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Katayose Y.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005428; BAD28635.1; -.
GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0003777; F:microtubule motor activity; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3ED39F5BA41561E6 CRC64;
                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                  707 AA
                      Pred. No. 6.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001372; Dynein_light1.
Pfam; PF01221; Dynein_light; 1.
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD005145; Dynein light1; 1
SEQUENCE 99 AA; 10617 MW; 3ED3;
75.0%; P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Cree 25-OCT-2004 (TrEMBLrel. 28, Last 25-OCT-2004 (TrEMBLrel. 28, Last Dynein light chain type 1-like. Name=P0693E08.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   uncultured archaeon GZfos1D1.
Archaea; environmental samples.
                                                                                                   15
                                                                                                                                                   11 EKARFFOAFKAAEAAA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      645 EKLKSEAERAAAAA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomics.";
Science 305:1457-1462(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EKAKFEAFKAAAAA 15
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                                                                                                 1 EKAK-FEAFKAAAAA
                  Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 73.3
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
ORFNames=GZ1D1 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=286721,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15353801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEERTS
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                                                                                                                                                                                                                                                                                                                  STRAIN=Oregon-R;
MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Warner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: Belongs to the ribosomal protein L22e family.
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Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Asp/Glu-rich (highly acidic).
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Pred. No. 52;
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                                                                                                                                                                                                                            Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein L22 (Fragment).
Name=RpL2; Synonyms=rpl22;
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FINESC, FBGN0015288; RpL22.
InterPro; IPR002671; Ribosomal L22e.
Pfam; PF01776; Ribosomal L22e; 1.
ProDom; PD007306; Ribosomal L22e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003418; AAF45546.1; -. EMBL; AL132792; CAB60023.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U42587; AAB17433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EKAKFEAFKAAAAA 15
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Best Local Similarity 73.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                     systematic review
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster.";
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Q9UAN1;
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Q9UAN1
ID Q9UAN
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DT 01-M
DT 01-M
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OS Droge
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                                                                                              SEQUENCE FROM N.A.
MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;
KOyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;
"Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal proteins, L22 and l23a, with unique histone-like amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-- SIMILARITY: Belongs to the ribosomal protein L19P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobianceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                     Gene 226:339-345(1999).

EMBL; AF080131; AAD19341.1; -.
FlyBase; FBgn0015288; RpL22.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR002671; Ribosomal_L22e.
Pfam; PF01776; Ribosomal_L22e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 62.3%; Score 43; DB 2; Length 312; l Similarity 73.3%; Pred. No. 55; 11; Conservative 0; Mismatches 4; Indels
                     Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L19.
Name=rplS; OrderedLocusNames=R03246; ORFNames=SMC03863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Ribosomal protein.
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                                                           NCBI_TaxID=7227;
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28-FEB-2003
                                                                                                                                                                                                         extensions.
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Q92L39;
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HAMAP; MF 00402; -; 1.

Gaps

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Indels

Length 179;

60.9%; Score 42; DB 1; 66.7%; Pred. No. 48;

1; Mismatches

Conservative

Query Match Best Local Similarity Matches 10; Conserv

. 0

1 EKAKFEAFKAAAAA 15

8

HAMAP; MF 00402; -; 1.

InterPro; IPR01857; Ribosomal L19.

Pfam; PF01245; Ribosomal L19; 1.

PRINTS; PR00061; RIBOSOMĀLL19.

ProDom; PD002979; Ribosomal L19; 1.

TIGRFAMS; TIGR01024; rplS bact; 1.

PROSITE; PS01015; RIBOSOMĀL L19; 1.

COMPlete proteome; Ribosomāl protein.

SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;

DR DR DR DR SW KW KW

PIR; AF2908; AF2908. PIR; F97683; F97683.

us-10-056-583a-95.rup

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MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
WEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
A Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
A Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Relanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Renome sequence of the plant pathogen and biotechnology agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21608550;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Sanphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=rplS; OrderedLocusNames=Atu2703, AGR C 4900;
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                          60.9%; Score 42; DB 1; Length 177; 66.7%; Pred. No. 48; 4; Indels :ive 1; Mismatches 4; Indels
InterPro; IPR001857; Ribosomal L19.
Pfam; PF01245; Ribosomal L19; 1.
PRINTS; PR00061; RIBOSOMĀLL19.
ProDom; PD002979; Ribosomal L19; 1.
TIGRFAMS; TIGR01024; rplS bact; 1.
PROSITE; PS01015; RIBOSOMĀL L19; 1.
Complete proteome; Ribosomāl protein.
SEQUENCE 177 AA; 19255 MW; 1BD19D6561AB8F22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
508 ribosomal protein 119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 EKARIEAEKVAAAOA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                              1 EKAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                       Local Similarity 66.7
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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OSUBZS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Kaneko T., Nakamura Y., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

DNA Res. 7:31-338(2000).

-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).

-!- SIMILARITY: Belongs to the ribosomal protein L19P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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PRINTS; PR00061; RIBOSOMALL19.
ProDom; PD002979; Ribosomal_L19; 1.
TIGRFAMs; TIGR01024; rplS_bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
Complete proteome; Ribosomal_protein.
SEQUENCE 181 AA; 19927 MW; AEF19D6593A9E835 CRC64;
                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L19.
Name=rplS; OrderedLocusNames=ml14283;
                                                                                                                                                                                                    181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00402; -; 1.
InterPro; IPR001857; Ribosomal L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MAFF303099;
MEDLINE=21082930; Pubmed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP003003; BAB50976.1; -.
137 EKARLEAEKVAAAQA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.9%;
                                                                                                                                                                                                STANDARD;
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Best Local Similarity
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nes 11; Conservative
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                                              76 DPATFEAFKAATGVA
                        1 EKAKFEAFKAAAAA
                                                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29471;
                                                                                                                                                                                                                                                                                    protein.
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Q6D7F3;
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Q6D7F3
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     Gaps
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
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Summer E.J., Bomer M.L., Bean E.D., Embry A.E., Mebane L.M.,
Tsou L.L.-C., No E.-G., Gonzalez C.F., Young R.F.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY368235, AAR89355.1; -.
SEQUENCE 274 AA; 28795 MW; 14419D38C3112965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.9%; Score 42; DB 2; Length 386; Best Local Similarity 60.0%; Pred. No. 97; Matches 9; Conservative 1; Mismatches 5; Indels
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Pred. No. 71;
   4; Indels
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                          274 AA
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 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00909; SPERMDNBNDNG.
TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006059; SBP_bac_1.
InterPro; IPR001188; Sperm/putr-bndng.
InterPro; IPR006311; Tat.
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                                                                                                                                                                                                                                     Created)
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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                                         1 EKAKFEAFKAAAAA 15
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116 KAEIEADKAAAAS 129
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10; Conservative
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05-JUL-2004 (
05-JUL-2004 (
05-JUL-2004 (
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05-JUL-2004
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SEQUENCE
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Q6UK87
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QGW1S9
ID QGW1S9
DT O5-JU
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DT O5-JU
DT O5-JU
DE SPERM
GN ORFRA
OC BACTE
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Name-tolA; OrderedLocusNames=ECA1372;
Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SCRI 1043 / ATCC BAA-672;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15288952; DOI=10.1016/j.jbiotec.2004.03.020;
Hansmeier N., Bartels F.W., Ros R., Anselmetti D., Tauch A.,
Puhler A., Kalinowski J.;
"Classification of hyper-variable Corynebacterium glutamicum surface-
layer proteins by sequence analyses and atomic force microscopy.";
J. Biotechnol. 112:177-193(2004).
EMBL; AY525006; AAS20307.1; -.
SEQUENCE 508 AA; 55416 MW; B28137E469228581 CRC64;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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   395 AA.
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PRT;
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Search completed: March 31, 2005, 02:41:13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=ebig455; OmrNames=ENSANGG0000000430;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L., Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.; "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=PEST;
Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Vibrionaceae; Vibrio.
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Pred. No. 1.3e+02;
Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
EbiP455 (Fragment)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein VC1791.
OrderedLocusNames=VC1791;
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                                                                                                                                                                                                                                                                                                                             344 AA.
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                                                           3; Mismatches
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104 EQAAYEAFEAARARA 118
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                          60.08;
                                                                                                                1 EKAKFEAFKAAAAA 15
                          Best Local Similarity 60.0
Matches 9; Conservative
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Q9KR55
ID Q9KR55;
DT Q1-OCT--
DT 01-OCT--
DT 01-JUN--
DE HYPOCHE
GN Orderterion
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OC STRAIN--
RP SEQUENCI
RC STRAIN--
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RA Heidelb
RA Gill S.
RA Mekalan
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Q7QLQ4
ID Q7QLQA
DT 01-MADT 01-MADT 01-MADT 01-MADT 01-MADT 00-MADT 
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Gaps
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                                                                                                                                  Length 346;
                                                                                                                             Score 41; DB 2; Length 346
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
Nature 406:477-483(2000).
EMBL; AE004256; AAF94940.1; -.
PIR; C82156; C82156.
TIGR; VC1791; -.
Complete proteome; Hypothetical protein.
SEQUENCE 346 AA; 37684 MW; 8482E0264D91A6AA CRC64;
                                                                                                                               59.4%;
                                                                                                                          Ouery Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                      307 EAFKSAAAAA 316
                                                                                                                                                                                                      6 EAFKAAAAA 15
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